1000

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GGTGCGCAAA GGTTACCTTA GAGTGGTTGG AAATCACTCT GTAAGTGTAA AGGCATAAGG   2760

TAGCTTAACT GTAAGACTGA CAAGTCGAAC AGATACGAAA GTAGGTCTTA GTGATCTGGC   2820

GGTGGCAAGT GGAAGCGCCG TCACTTAACG AATAAAAGGT ACTCCGGGGA TAACAGGCTT   2880

ATCCTTCCCA AGAGTTCACA TCGACGGAAG GGTTTGGCAC CTCGATGTCG GCTCATCGCA   2940

TCCTAGGGCT GGAGCAGGTC CTAAGGGTAT GGCTGTTCGC CATTTAAAGC GGTACGCGAG   3000

CTGGGTTCAG AACGTCGTGA GACAGTTTGG TCCCTATCTG CCACAAGCGT TGGATATTTG   3060

AGAGGAGCTA TCTTTAGTAC GAGAGGACCG AGATGGACGA ACCTCTAGTG TrCCAGTTAT   3120

CCTGCCAAGG GTAAGTGCTG GGTAGCTACG TTCGGAAAGG ATAACCGCTG AAAGCATCTA   3180

AGTGGGAAGC CTTCCTCAAG ATGAGATATC CTTTAAGGGT CCTGGAAGAA TACCAGGTTG   3240

ATAGGTTAGA AGTGTAAGTA TAGCAATATA TTAAGCTGAC TAATACTAAT TACCCGTATC   3300

TTTGGCCATA TTTTTGTCTT CCTTGTAAAA ACCCTGGTGG TTAAAGAAAA GAGGAAACAC   3360

CTGTTATCAT TCCGAACACA GAAGTTAAGC TCTTATTC                          3398
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(2) INFORMATION FOR SEQ ID NO: 36:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 3203 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

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GAGAAACCAA GAATTAAATG TAAAAATAAA GATCGTTTCA TAAAGATTGA AAAAGAAAAT    60

GACAAAACAA TGTATCATAC AAAAATAATG ATGGATATTT ATAAATTAGG AATTGACAAT   120

AAAAGAAATG AATGTCGTAT ATCATTAAGA ACACTATTTA ATCAAATGAA AGTAGAAGAA   180

GTTCGTTTAT ATTCTATAAA AGAAGGGGAC AAATTTTTAG GTATTTACTA TGGATATAGA   240

AAACCTATAA AAAACATTTT CGTAAAATAT GAAATAAACG GAACCATAAA GTCATATGGA   300

TTATCAAAAG CACATTACAT AGAATTTAGA TTTAAAAAG GAAGCGTTTT TTGTTACTTT   360

AAAGGATTAT TTCGCTTATT AAAAAAAGAA AAAGAAATA CACCATATAA TATGGCTTGT   420

ATTGATATGT TTACAAAACT AGAGAAACAC GTATATGAAT TTTACGGTAA AAAATATCCA   480

GAAAAAGGAA TAATTATAAG ATGGATAGAA AAAAATCAAA AATAATAACA ATTGCAAGCC   540

TTAAAGGGGG CGTTGGTAAA AGCACAACTT CAATAATACT TGCAAATCTA TTATCGAAAA   600

AGCATAAAGT ACTTTTGATC GATACAGATG ATCAAGCTGC TACTACAAGC TATTATTATA   660
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1001

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ATGAATTAGA AACAAAAAAT TTCGATATAT CTAAAATGAA CATAGGAAAT GTTATAAAAG        720

ACGGTACAGA TATTAATAAA AGCATTATTA ATGTTGAAAA TAACATAGCT TTGATACCCA        780

GTTATATAAC AGTCGATGAA TTAAATGGAG AGTATTATTA TGATAACCGG CATCTTCCAA        840

TTGAATTTTC ATTAAAGACG AAATTAAATT CCATAGCAGA CAACTATGAT TATATTATAA        900

TTGATACTAA TCCCAAAAGG AATTTCACAT TAAAGCTTTC CCTAATTAGC AGTAATTATG        960

TAATATCTCC AATGACGGCA GAAAAATGGG CAGTTGAAGG ATTTGAAACA TTAAGAAGGT       1020

ATATAAAAGA AGTTGCTGGA ATACCAATAT TTATTGTTAT TACAAGGTTT AAAAAAAATG       1080

TTACCCACAA GCAATTAATG GAAATAGTAA GCATGAAAAA CGGGTTTTTG GGATACATAA       1140

GCGAAAGAGA AGATTTAAAT AAAAGAATAG GGTGTAATGA AAAATTTGAT TTTTCAAAAG       1200

ATTACATTAT TGAATATAAA AAAATATTGG ATGTTTTTTT GGGAAAATTG TAAGAATTGA       1260

CAAACTTAAT AAGTCCGGCA TGCCGGACTT ATTGGAAATA AGGGCAAAAA TATGAATAAA       1320

AAAAACATTA ATTTAAAAAT TAATAAAAGA ATTTCAGAAA ATAATTTAAA TTATATTCTT       1380

GATCAAAGCA ATGAGAATCA AAGAAAGAA GAATTTGAGC GATTAATTAC ACAATTAAAA        1440

AATAATATTA AATCAGAAAT ATACAATATT ATTGATACCA TGAAGATCCT TAAGAAAATA       1500

AATGACAAGA GGCTCTATTT AGAAGGAGGA TATAAATCTT TTAAAGATTT TTTATCAGAT       1560

TTTAAATTAG CAAAGACACA GTCTTATGAA TATATAAAAT TAGCCGCTGC AATTGAGGCG       1620

GGAATATTAG AAAGAAAATT TTATTACCAA TAATGGAATA AGGGCCTCTA TAAGATATAT       1680

TAAAAATCAA GCAAATGGTA CAATAAAAAA ATCAAAACAA AATCCAATAA AACCATTAAG       1740

ATTTCAACTC AAGAACCAGG AAAGTTATGA CTTTTATAAA AGCAATTCTA GGTTTGTAAG       1800

TTTTATGATG GATGAGATTT TTAAAAATCA AAAAGATTTT CTTAATAAAC TTTTAAAAAG       1860

ATATAAGGAA TCAAAGGGAC AATAAGAAAA TTTTATAAGC AATTTAATCT TTAATATTAT       1920

TGAAATATAA AATATAAAGT TAGAAATTGT AAATAATTGA TTTAACAAAT AAGGAAATAT       1980

ATACAAAAAA GCAACTGAAA ATTTAAAAGA TCATTTGCTA AGCAGAGGAA TTTTATTTGG       2040

TTAAAGTATT TGAAAAAAAA TTAAATATTA TCAAAGAAAA AGGTAAATTG ATCTCAATTG       2100

ACAATAAATT GTCAGTAATA AGCAACGAAG AATGTTTTTA ATTTTGATTA TAATAAATTT       2160

TGCAAAGAAG CACGCTTAAT AAGCACGGTG TAATAAGTTG GGCAATATCT TGATTAGCAA       2220

CAATGTGTTT TGATAATCAA TGGTAAGACG AACACTTAAA AATATTTTAG AAGGAACAGG       2280

GCATTTAAAG TAAATTTATA TATATTTAAG AGTAAGGATT TGAATAATTT ATGATTTAGA       2340

GCTGTAGAAT TTATTAAAAT ACAAGAGCAA CTATTAAAAA AATGGGCAAA TTAGAAACTT       2400

TAGCAGGGGT AGTGATTTAT AAGGACGGGG TGTTAATGAC GATATTATAT AGGCTCAAGG       2460
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GCCAGCAAGG ACTACTATTG ATTATATAAA CACTGTTGTT TAAGATTTTA AAAAAAAGAG    2520

GCTATTTTAA AATAACAAAT ATTTTATAGA ATTTATATTC AAGCATAAAT TTAGGAATTA    2580

AAATCAATGA GTTTACTATG AATCTTGAAT TTGTTTTGTT AAATTCAAAA CCACCACACC    2640

CCTATTTTTT AGCTATCTAA TTAAGGGATC CATATGTGTC CCCTTTATTT TTAAATAAAA    2700

GATATATATT TAAAGACAGT TAGGCCTCTT TTAGGCATAT TTTTGTTTAA TAAAAAATAT    2760

TAAATTAGGG TTTATAATTT TTATAGATGA AAATAAAATA GAAGAATCTA ATTTAACTAA    2820

ACAATTTTTG TTTAGTTAAA ATGATATAGG GCTTTGCAAA GTAGATATAA TTAAAGAAAA    2880

TCTAAAATCG CTAAATAAAA CTATTTAAAC TAAGCCCCAT AATGAAAAAG TTTTAGTAAA    2940

AATATTAAAG AATATTTTTA CTAAAATAAA AATTAAACCA GCATTAATAA TACTTACATT    3000

AGATGATTAG CTACTTTTTT TAATTAATAA ATTTTGCATT TAAAGTTCTA TTCCACTTAT    3060

AAATATTGAC TATATCAATA ATTTTTCAAG CATTGGTACA TTTTATATTC TAAATATTTC    3120

GTTTTGTCGC TAATTTGTTG ACATAGGAAT TATAAAAAGG CCATCATCTT TTAAATTAAA    3180

                                                                      3203
AAGTAAAATA ATACTAATAA ATA
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(2) INFORMATION FOR SEQ ID NO: 37:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3189 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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TTGCTAAAAA TATATTTTTT TATATCTtGG CTCTACTACA ACTCCTTTAT TTTTAGAGTA      60

ATAAATAAAT CTGCTGCCAA ATAACCTATA AGATATTTTT TAAACATAAC TTGGATCGAT     120

ATTTATAGAT TTAAAAATTT TTAAATCTAT AATAACTTCC AAAATACAGA ATCTTCACCT     180

AGATTATAAT TGTTTATAGC ATATTCTTCT TTTGAATATG TAAATTCTTA AGCTTATTTA     240

AAAGCTTTTT TCTTGTATAG TCAATTAGCT ATTTTAGCTT TTCTGGTTTG AACGCCAATA     300

CTAAAATTAT TGAAATATC TTTTAAAGAA ATCCCATTGT CATAAATATC TTTATTTGAA     360

AAATCTTTTT AGTAAAAAAA TAATGGGGAT ATTTGTATTC AAGTTTTTCA AAATTAATAG     420

TAAAGATATT GTTTTTTCCT AAAAACCCAT ATTTTTTTTC TCTTTTGCCT TTAATACTTT     480

TGTAAAATAC TTTAATCAGC TTACTTTTTT TAGTCCATCT TATATTTAGT AAAAATAGCA     540

ATAGTAACTC CGGTTTGGAT ACAAAATACA TTCTCACCTA TACTGCCATC ATCAGTTTTT     600
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1003

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TTCTTTCTTG AACTATCGTG TAAATTTAAT ATATAAATTT CATCAAATGT TTTTAAGAGG    660

TAATCTCATA CCTCTGAATG CCACCTTGTC AAGGTATCCA TTTGTTTGTT ATGATACCTA    720

GCAATCCTtC GTTAGAACTT TTAATTCTAT GTTCTGCAAA TCTAATAAAC TTAGTGCGGT    780

CATCATTAAG TGGCCTTAAA TTTTTTTCAT TTATAAACTT ATTTTCTATT TTTTTATAAT    840

CATTAACTAA ATTTAATATA TATTCATTAT TATTTTTTGA ATCTGAATTA TAAGGAGGAT    900

TTCCCAGTAT GACAAGTATT TGCTTTTCTT TAGCTTTATT TGTAAGTTTA TTTTCTTCTC    960

CAATTGCAGG GAAAATACCT TAAAAGATTT TTGATCTGAA GGGTCTGCTT TATCAATAAA   1020

ATTAGTCAAA AATATTTATA ACTTTATGTT TTCATTATTT AAGCTGTCGC TACAAATTTT   1080

TCTTTCAAAT ATTGACTTGG CTTTAAATGA TCAACTACAT AAGGAACCAT TAAACATTCA   1140

AAACCATAGA CATTTTTAAG TATGTGAAAA TTAATGTAAT CTTCTTGTTT TTCAGAGTCT   1200

ATTGGAATTT CGTTTAATAT AATTTTAATT ACTTCAGGTA AAAATGTGCC AATACTTATT   1260

ACAAAATCAA ACACTGCAAC TTTATCCCTA TTTTTAAAGC CATAATTTAA TTTAATTTTT   1320

TTAAGTGCCT TATGTAAACT GTTAACAATA AAACTTACAC CCGAATAGGA AGTGTACTAC   1380

ACTCCTTTGG CCTTTCTTAA TTTAACATCG TACTTAGCTA GAAAATCCTC ATAAAAATAA   1440

AGATAGGGGA TCTTTTGAGC TTGTTTTGGC TCTTGTAAAA GAAAATTCTT TAAAAAATAA   1500

GCTCTGTATC AATTTATTTA TTACATTAAT AATTTCTTCT AAAATCTATC TTGGACTATT   1560

ATATTCATTA TTTGTATCAA TATCACTAAT TAATTTTAAT ATATCTCTTA TAAGCGAAAA   1620

GTTAGAAAGT ATAAACTTTT TAATATTATA AAAAGCTATT TTTCATTAAA TTTAAGCAAA   1680

GACATAATTA CCTTATCTTA AACTTTTAGA TAATTATAAT TGATTTTTAA GGAAATCAAA   1740

ATGATGCCCC AAAAGCTTTT AATAATAAAA AATTGTTATT CTTGCCAAAA GCTACTTAAG   1800

AAAAATAGTA AAATTTGTTG TGTTGTTTAT AGAACTAGAA ATAAATACCC CAAAACCCTT   1860

ATAACGAGCT AATAATTGTT TTTATTGGGA GGTTATTTAG GGATTGTAAA TTTTTATATA   1920

CAAAGCCTAA AACAAATTTT ACATTTTTAT ACTCATATCC TTTTCTATTT CTTGCTTGCT   1980

GTTTCTTTAT AATAACGAGT TTTTAATCAA TTAAAATAAA ATTTTTCTTT CTAACATCTT   2040

TCTTTCTTCT TTCAAACCAT CTTCmAGACA CTTTAATTTA TCTTTATAAC TCTTCtTTAT   2100

CTTTTGGTTA TTCtTCtTTT TTAAATTTcT CTTACTTTTT GTATTcTTTT TCAATCTTTT   2160

CTAATTCTTG TATtCCTTTT TTATTAACTT CTAATCTTAG ATTTTCAACA ATATTTTAAG   2220

CTACCAGATT TTTAGATTTC TCTTGTATCT CTGCTTGGCA TCTTAAATTA ATTTCTCTTT   2280

TATCTCTTCT TTTGTATCTA TAAAATCTAA AAATTCTTTA GCTTGTTTTT TTAAATCTTA   2340

TTCTAAATTT TGTATATCTA CAACTTATAT AATGTTTATA AGAACTTATT AATATAAAAA   2400
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TAGCAGACAT AGTAAACTTT TCCTCATAAT TATCCCACCA AGCTTTAGGA ATATATTAAA    2460

TACCTATATT TACATATATA AAGCTTAAAA GCAATTTAAT TACATTGCAC ACTATAAAGC    2520

AAAAAAATAA AGCCCAAAAA AACTACTCCC CCCAGAGCAC AAATTCCAAA ATCACCAAAG    2580

CAGATCACAA TAAAGACAAT TAAATGCAAA CAATAAAAAT ACAAGATATT CCAACTTTAT    2640

TTAATAAAGT TGGAATAATT TTTTGCAACA TAAATTTTGA AAGCATTATC AAAATAAACA    2700

TTTATTAATA AAATTGTAAA AAGAAAAAC CGATATTAAA TACAAAGCTC AAATATCTAT    2760

AAGTTAATTT AGTTTTACAA CAACTAGCAA TAAAACTACA TTAATAAAAT TAATAGATAC    2820

ATTAAATTTC AAATCTTCAT TACAGACACT ATAAAACAAA ATTTTGTATT TTACTTTTTC    2880

TTATTATTAT ATTAGTTACA ATATCAAGCA AAACATCTTT TCTATTCTAA AAAGCTCCTT    2940

AAAAATATAA TTTACTATTA TTATCTCTTT TTTACAAACT CACATAATTC TTTATCTCTC    3000

ATGAAAATTC TAATAGAAAT ATTCTTATTA TTTAATTTAC TTATATGATT ATTAAAATTT    3060

AATGATTTTT TTTCTAAACA TGTGTTTTTT TATATTTTTA AATCCTAATT CCTTAATCTT    3120

ATCAATAGAT AAAACTATCC TCCAAAACTT TTGACTAAAG TTTTAAATAA AAATAAGTTT    3180

                                                                      3189
GCnTTTAGC
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        (2) INFORMATION FOR SEQ ID NO: 38:

                (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 3130 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

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TTGTAAAAAG TTTTGTTTGA TATAAGTTCA CTTGTGCCCT TTACTATTTT TGTAGTTGCT     60

TTTACTTTCA GCTTCATTAG CAGTTGCAAG TTTTTTCATA CATTCATAGT AAAGCTCCAT    120

TTCTCTTATT GAACACTCCT TTATATATTC ATCAAGCTCG CTTTTTAAAG AATTAATTTC    180

TCCATTAACA ACTTGCTTAT TTTTTTTACT ACTTGCTTTA TTTAAAGCGT CAATTTCAGC    240

TCTTAAATTT TCTATTTTAG TATGCATACT AAAAAGCTCA ACACTAGAAT ATTGCTTAAA    300

TGCATTTATA AATCCTAATT CTAAATTAGC CCGCTCTAAA TCCAATTCGC TTCTAACTTT    360

CCTAGCGTTA ACTTCTGATT TAAAAGTTTG CGACAAAAGG TGTTCAAAAG TGTCTTCACT    420

AATTGATAAT CTAGAGTCAT CGCTAACAGA ATTTTCCCCA CTTTCCCATT TTTTCCTCAT    480

CCTCCACACA TTTACCCTAG AAACCCCCAA TTTATCCGCT ATTTCCCTAT CATCTAACAA    540
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1005

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TCCTTCTCTA AAATATGCAA CATAATCATC AAAAGACCTT TTAACTTTTT TCAAAAAATC      600

CTCTAAAATA ACAAAATTAA CAAATTGTTG CTCTAAATAG TAAAGCAATT TATCAATTGT      660

TAACATTAAC TATTGTCTTG TTGATATCTA TTGACCACAG ATCTATCTTT ACAATTCTTA      720

TTAAACATGA ACCAGTATCA TTATTGTCGC CATTAAGAAG ACCCCTCATA AATTCGTTAG      780

CATTTAAAGA AAATAAAGCA AATATAAAAT AATATAAATT CTTTTTATTT ATCATGATTC      840

TCCAATATTA ATAAAATAAC AAGACTAGTA GCTAATCTTG TTATTCATAA TTTATGCTTA      900

TAAAAACCAT TTATTTTATT TCGAAATCTT TTTTAGCTTT TCTTAATAAA TATCTTATAA      960

GATTCTTTTT TCAAATTAAA ATCTAATCTT TGGGCAAATC AGCCAAAATT TGTTTTAAAA     1020

TTTGTTTAAC TGTATTTGCT TTATCTTCAG AATAATCTTT TTTAAAATTA TTTCTGGCGT     1080

TATCTCCATA TTTCTCAGCA TAATCAATTT TATCCGAATT TAATTGTATC AAATAATTAA     1140

AAATCGAATC TGGATAACTC CCTATAAGTC TAATCATATC CTCAGACAGG AAAATACTAT     1200

CAGTACTTAT CTTAATTTTT ATAAGATATT CAATAGCCTC AAGAGCGTCC AAAAAAACAC     1260

TTTTTTCTTT AATTCCAATT TTTCTTAAAT CTCCTCTAAT TCTAGGAGCA TCGGAAAAAA     1320

CATGACTTTT TTCATACTCA TTTTTAAAAT CATAATTATC TAGTCTTTTA TTTATTAGGT     1380

TAAAATCTTC TTTAGAAAAA GCTCTTTTAG TTTCTGTATA ATTTTCTTCT ATATTTGCAC     1440

TTAAACTTAC TACAAATAAA AACAAAAATA TTAACAGACT AATTTTTTTC ATATCCCCTC     1500

CTAGCTTTAT TGCCTAAATT TCAGCAATGT AAATGCTAAT AAACAATAAG ACTGATTGTT     1560

AGTCTTGTTG TTTATAATTT TTACTATCAA AACCCATTTT TTATTATTTT TTATCTTCTA     1620

TATTTTGAGG CTCTGCTAGC TTTTCAAGTT CTTCCTCAAT ATTTTTAAGA GCATCATCTA     1680

TAACCTTTTT TACAAAATCA TTAGTATTAG TACCATCATT AACAGAATAA CTTCCATTTA     1740

CACCCAATTC TTTAGCATAC TTTAAAGCTT TTTGTCCAAT ATTTCCTTGT TTTTTAACTT     1800

TCTCAGTACT TTCTCCAGTT GCAGATTCAA CTTGTTCTTT AAATTCTTGA AATTTCTTTC     1860

TAGCCTCTTC TAATTCTTTT TTTCTTTTAT CTATTTTATC CTTTAATTCT TGAATTTCTT     1920

TTTCTTTCTC TTCTTTTCCT TCTTGTTGAC CACCATCTTT TGCTTGCACC GCTTTTAATA     1980

CGGGTGTGTT ATCGTGGGAA CTTGCCGGCA ATACTGGTGG TGGATTAAAC AGACTGTTAT     2040

TAGGATCGTC ACCTTGCATT AACTCTTTAT CTAAAAATCC TTCAACTTTT TCTTTTACAT     2100

TTTGTTTTAA ATCTTCACTA CTCGCATCAA TCTTGCAAGA AATTATCAAA ACAAAAACTG     2160

CACAAATAAT TAAATTTTTC ATTTTCTTAT TCATAAGTTA CTCCATAAAG TACTAATATT     2220

ACCACAACAC CAAATAATTG CAATATTTCA AAGATTTAAA TATATAATTT TGTTACATTC     2280

AGCTGTTACA TTTTAACAAA ACACAAATGT AATTTTAACC AACTCGCCAA AATCTCTCCA     2340
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TTGCAAATGC TCTACTCATT ACAAAGATT ATAAAATACA TACAAATTAA ATTTTCAAGT   2400

CTTTGCTATA TATTACACAA AGTATACTAT CTTTCTTGTG TACCACCCTC AAAAATCACT   2460

ACTTCTGTTT ATTACACCCA CTCTACAGCC CAGATTTTGC ATGCAATGAG AACACTCCAA   2520

ATTTGACTAA AATTTTTCGT TTTTAGTAAA ATATAATTTA CATTTTTTAT CTATTTTTAT   2580

TACTTTTACT TAATTTAAAA GTAACAACTT CAAGGAGAGG ATTTTATGGA CAATAATAAT   2640

TCTTTTAATT TAAATAATTT CAATATGGAT TTTACGCTCA AACTATTTCA AGAATACCAA   2700

AAACTAATAA ATGAAAACAA AATTCTTAAA AATTCACTAA AAAATTCATC TAAAAGTAAA   2760

AAAGAAAATT CAAAACCAAC TCCTAAGTTT TATTTAACCC CTAAAAGTAT TAAATTAATT   2820

CTAAAATGTG CCAAAACCTT AAAACAAATT GACCCAATTT CTGGTTGGTT TGTGCATCTA   2880

CTCTTAATAA GTGGATGTAG AGGCACTGAA ATGCAAAAAG TAAAAATGCA AGATATTTCA   2940

ACTTTTTTAA GCAAAACCGG AAAAACTTTA TATACTATTA AAGTAAATGT GGCAAAAAAA   3000

AGAAATACCT CTTGTATTAG AGAAATTGTC ATCAACTCAG AAGAGTTCGA GGCTATCCAA   3060

ACAGCACATA AAAATCATTT CCAAGAAAAA ACTCTTGACT CAAGGCGTAC TTATCTTTTC   3120

CAAAAGAGCA   3130

(2) INFORMATION FOR SEQ ID NO: 39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3029 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGTTTTCCCA TTTCGCTCCG TAACTTGTGA TTACACTATC ATTTGmGwcy CCTGATATkT   60

cTGTGGAkaT TATTGTTgAA GmTTTTCCtC TTTTcCTCCT TATTTTGTAa TAAaTAtTAT   120

ATgCAAAAAC TATTTTTGCC AACTTTTTTA CAAAAAATTT TACAAAAAAT TAGTTGGGCT   180

TATTTAAATT CTCTTGTTAA AGAACTTAGC TAAACCCAAC TTAATTGGAT TTTTTTGATA   240

GCAATATATT TTTTTAGTTA TACATATACA TATGTATAAC TAAAACTATT TTTGTCAGGC   300

TTTTTACAGA AATTATTATA ATAAATAAAA GCTTTATTAA ATTCTCATGT TAAAGAGCTT   360

AATAAAGCCG CGGGCTTAGC TTAATTTATT TTAGATAAAC TCACTAAACA ATTAAATTCA   420

GTTCAATTTA GAATTAAAAT TATTTTGTAT TTATTAAAAT AAAAGAACCT ATTTAAATTA   480

TCTTGTTAAA AAATTCAAAT AAGTTCTACT TTAGAGCTAT ATACTAACTT ATTACTTTAT   540

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AAAATTTTAA TCATTTTCAA TTGAAAAAAC ACTTATTAAA TATAGAATAG ATAATTGGGG     600

CAAACGTTAT TCCCATTATT AGAATTACTT GTATTGTTCT ATTGCTTGCA TTAAGTTCAT     660

TTTTTTAAAT ATCTATTTTA TTGTCTAGAC TAGATATATC TTTTTGCAAA GTTTTTTCTA     720

CACTATCTAT TTTAGTATTT ACACTATCTA TATCTTTTTG AAAATTCTTT TCTACATTAA     780

TTATTTGTTG TTCTAAAGAA TTCATTTTCT CCTTTAAAAC TTCAAAGTTG TAATTGTCGT     840

TCTGAAGTAA AACAAAATCT ATTGCCTCTT CACTAAACCC CTTATTTAAA AATTCTAACC     900

TTATATTTTC TATTTTAAGA GCATTGTAGG CTAAATTACT CATAAAATCC CCTTTATTAT     960

CCTTTTAATT CTTTATATTT TTTTAAAAGT TTATTAATCA AATCTTTTTG ATTTTCAAAA    1020

ATCTCGTCCA TCATAAAACT AGTAAATTTG GCATTTTTTT TATAAAAATT ATAACTTTCC    1080

TGTTTTTTAA GTTGAAATCT TAGGGGTTTT ATTGGATTTT GCTTTGACTT ATCCTCTTTA    1140

ATTTCTACGT TTAATATATT TCTATATACA CCCTTTAAGC CTTTTTCTTT AATATCATTT    1200

ATTGATATGC TCCCCTCTAA TACTTTTCTA TAAATTTTAA GGTATAAAAA AGCCTGACTT    1260

CTAGATATTA TAAATTCTGA CAAAAAGTCT TCAAATTTTT TATAACCATC AATCAAATAA    1320

AGTTTTTTTT CTCTTATTTT ATATAGGATT TTCATTGTTT TAATTTTATT CTCAACATCA    1380

TCAACAGTAA TTCTACGAAG TTGATCCTTA TAGCTTTTAT ATTCAAGTTC CTCATTTTCA    1440

AATTCTTGAA CATCCTCAAT TCTATTATTT AATAATATTT TTTTTACTTT TAACTTTGAC    1500

ACTTAATCCT CCTAAGTTTC TGATTTATTT TTAAAAGTCT TCCGGAAGAC TTTTAAAACA    1560

TATTGTTTAA TATTTTTTTT ATTTCTTGAT AATAAATTTC TTTATTATTA GGCTCTTTCA    1620

ATTCATTTAT AAAAACCTTA ATTGAATTAT AAAAATGAAC TCTTCCTTTA ATAAGATCTT    1680

TGTATTCTGA CTGCAAAATA CTTTCAATAT CTTTATACGT ATTTCTATTT TTTATAAATT    1740

GATTTCTAT TATTAACACA TCAATATTTT TCTTTCTTAT TATTTCAACT TCCTTTATTT    1800

CATTCATTAA TATTGGCAAA GACTCTACAG ACCACCTTTC TGCTTGAATA GGTATTATAA    1860

CTTTATGTGT AATGTTTAAC GCATTAAACA ATAAGAACT TAAACTAGGG GGAGTATCAA    1920

TTACTACATA ATCAAAATTA TAATAATGTA AATTTTTATC AAATATATGT TCTAACATAA    1980

GCTCTTTATA AGGAATATCT CCTTTTTCAA ATTTACATAA AATTGGATGG GCCGGAATAA    2040

TATACATATT ATTATTTATT GAATTTATAT ATTCATTAAA AGCAATGTTT TGATCTCTTT    2100

TTAAAAGATA ATAAACATTA TTCAATTCAA TATTTCTGAT ATATTGTAAA AAATAACTGG    2160

TTAAACTATT TTGAGGATCT AAATCTACAA TCAACACTTT ATTGTTCATT TCGCTTAAAA    2220

TATATGAAAA TATAATTGAC AACATGCTTT TGCCAACACC GCCCTTAATT GACGCTATTG    2280

TTATTATTTT AGGTTTTTTA TTATCCATTT TATTAACGGT CCTTGTTCTG GGTATTTTTT    2340
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CCCATAAAAT TTATATACTT GTTGTTCTAA ATCTGTAAAC ATACTAAATA AAACTTTGTT        2400

GTAATGATTA TTTGTTCTTT TTTTATCTAA TAATCGATAT AATCCCTTGA AATAGCAAAA        2460

TACACTTCCG GCTTTAAATC TAAATTCCAT ATAATATGCC CTTGCTAATG CATATGCTTT        2520

TCTAGTTCCr TTTATTTkAT ACTTTATTAA wGGyTTTTTn ATTGGTTTTC TrTAGCCATA        2580

AAAAATACCA ATAAACTTAT CTCCTTCTTT AATTGGGTAy AArTGAGTTT CTTCAACAAT        2640

yCTTTCCCCA TTAAATAGGG CCCTTAATGA TAGTCTAAAT TCATGTTTTT TTTCATATAC        2700

TCCAAATTTG TAAATGTCCA TCATTATTTT TGTATGGTAC ATTGCTTTAC CATTTCTTT         2760

TTCAATTAAA ATAAAGCGTT CTTTATTTTG ACATTCAACT TTACATTTGC CCTTTTTTAT       2820

AGTTTCAATA GGCTCCATTG CACTTTCCAT ATTTAAATCC TCATATAGCC TTTATGTTAA       2880

ATTCTTCTGT GGTTAAAGAA TTTTTTTGTT TTCTTATTAT TTCCAATAAT TCAAGATAAT       2940

ATGTACCAAA TACTTTATTG TATTCTATTT TCTTTTGGTT ATTCAAATAT TTTTTGGTAA       3000

TTGGCTTTAG AATTTCAATA TTTgTTTCC                                         3029
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(2) INFORMATION FOR SEQ ID NO: 40:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3000 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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CnCACAGnAC CTTTTAAAAG AGTATTCTAT TTTCTTAATT TATAAAAAAA TAAAATCAAG          60

GTAAGAACTA TTTAAAATAA ATCTTGTGAA TCTTTAGTAG TGAATGATTG TCTGTCCTAG         120

TAACTTAGAA CTTAGAAAGT TAGCAAAGCA AACTTTCCAT CCTTCTTCAT CTCATTACCA         180

AAATCCGCAT CCTCATCACC CTTTCCAATA GCAGCAGCAA TCGGATTTGT AGCCTCCCCA         240

GGCTTCTCTC CATCCTGCTC AGCCTCACCA GCAGCCTTAA CAATCGCACT TAATATCTGC         300

TCCCCACTAA CAGCACCAGC CGCCTTGCTA GCAGCCTCAC TGTCCCCAGC ATTAGCATTA         360

TCAACTTTCC CAAACAACTT CCCTGCCTTT TTATTATTCT CCCCTGCAGC AGCAGCAACT         420

TTCAGCTTTT CACTCCCCCC AGCAGCTTCA ACAATCTCCT TTATTCCCTT AGCAATCCCC         480

GTCACACTCG CCTCATCAGC AGCCTTCGCA GCACTATTAT CAGCCACAAC TTCTCCAATT         540

GCATCAGTAC CACTTGAAGC CCCCTCAGCT GTCTTTACAC AGCTTTTACC AGCTTATCCA         600

ACAACTCGCT AACTTCTTTA ATAGCCCCCT CAGCCTTCTC TTTCTCACCA CCACCACTCT         660
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1009

TCACAGCAAA CTTTCCATCC TTAGCCATCC CCCTCAAAGC AATAGCAGCA GCAATCTGAT   720

CATCCTTCTT CATCTCATGA TTAAACTCCG CACCCCCATC TTTATCCCCA ATAGCAGCAG   780

CAATCGGATT TTTAGCATCC TCAGGCTTCT TTCCCTCCTG ATCAGCCGCA CCAGCAGCCT   840

TAACAATCGC ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC   900

TAGCAGCCTC ACTGTCCCCA GCAGCAGCAC CAGCCTTCCC AAACAACTTC CCTGCCTTTT   960

CATTGCTCTC CCCTTTAGCA GCAGCAACAG CTTTCAGCTT TTCACTACTC CCCCCAGCAG   1020

CTTCAACAAT CTCCTTTATC CCCTTAGCAA TCCCCGTCAC ACTCGCCTTA TCAGCAGCCT   1080

TCGCAGCATT ATTATTATCC ACAACTTTTC CAATTGCATC AGTACCATTT GAAGCCCCCT   1140

CAGCTGTCTT TACAGTTGTT ACCAGCTTAT CCAACAACTC GCTAACTTCT TTAATAGCCC   1200

CCTCAGCCTT CCCTTTCTCA CCACCACTCT TCACAGCAAA CTTTCCATCC TTAGCCATCC   1260

CCCTCAAAGC AATAGCAGCA GCAATCTGAT CATCCTTCTT CATCCCCTCC TTATTAAACT   1320

CCGCACCATC ATCCGCATTA CCCTTCCCAA TAGCAGCAGC AATCGGATTT TTAGCCTCCT   1380

CAGGCTTCTT TCCCTCCTGC TCAGCCGCAC CAGCAGCTGC AGCCGTAACA ATCGCACTTA   1440

ATATCTGCTC CCCACTAACA GCACTAACAG CACCAGCCGC CTTGCTAGCA GCCTCACTGT   1500

CCCCATTAGC AGCATCACCA GCTTTCCCAA ACAACTTCCC TGCCTTTTTA TTATTCTCCC   1560

TTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCCAGC AGCTTCAACA ATCTCCTTTA   1620

TCCCCTTAGC AATCCCCGTC ACACTCTCCT TATCAGCAAC CTTCGCAGCA GCATCATTAG   1680

CCACAACTTC TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACACAGC   1740

TTTTACCAGC TTATCCAACA ACTCGCTAGC TCCCTTAATA GCCCCCTCAG CCTTCCCTTT   1800

CTCATCACCA CTCTTCACAG CAAACTTTCC ATCCTTAGCC ATCCCCCTCA AAGCAATAGC   1860

AGCAGCAATC TGATCATCCT TCTTCATCTC ATGATCAAAC TCCGCACCAT CTCCGCATC   1920

ACCCTTCCCA ATAGCAGCAG CAATCGGATT TTTAGCATCC CCAGGCTTCT TTCCCTCCTG   1980

ATCACCAGCA GCCGCACCAG CAGCCTTAAC AATCGCACTT AATATCTGCT CCCCACTAAC   2040

AGCACCAGCC GCCTTGCTAG CAGCCTCACT GTCCCCAGCA TTACCAGCAT CAACTTTCCC   2100

AAACAACTTC CCTGCCTTTT TATTATTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTT   2160

ACTCCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT TCACACTCTC   2220

CTTATCAGCA GCCTTCGCAG CAGCATCATC AGCCACAACT TCTCCAATTG CAGCAGTACC   2280

ACTTGAAGCC TCCTCAGCTG TCTTTACAGC TGTTACCAGC TTATCCAACA ACTCGCTAAC   2340

TTCCTTAATA GCCCCCTCAG CCTTCCCTTT CTCATTATTA TCCTTCTTCA CAGCAAACTT   2400

TCCATCCTTA GCCATCCCCC TCAAAGCAAT AGCAGCAGCA ATCTGATCAT CCTTCTTCAT   2460

CTCATCCTTA AACTCCGCAC CATTCTCATT ACCCTTCCCA ATAGCAGCAG CAATCGGATT   2520

TTTAGCCTCT GCAGGCTTCT TTCCCTCCTG CTCAGCCGCA CCAGCAGCCG TAACAATCGC   2580

ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC   2640

ACTGTCCCCA GCATGAGCAG CATCACCAAC CTTCCCAAAC AACTTCCCTG CCTTTTCATT   2700

GCCCTCTTTA GCAGCAGCAA CTTTCAGCTT TTCACTCCCC CCAGCAGCTT CAACAATCTC   2760

CTTTATCCCC TTAGCAATCC CCTTCACACT ATCCTTATCA GCAGCCTTCG CAGCATCAGC   2820

CACAACTTCT CCAATTGCAT CAGTACCACT TGAAGCCCCC TCAGCTGTCT TTACAGCTGT   2880

TAcCAGCTTA TCCAACAACT CGCTAGCTCC CTTAATAGCC CCCTCAGCCT TCCCTTTCTC   2940

ATCATCATTC TTCACAGCAA mCTTtCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC   3000

(2) INFORMATION FOR SEQ ID NO: 41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2991 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAAAAAAC ATGAATTTAG ACTATCATTG AGGGCCTTAT TTAATGGAGA AAGAATTGTT   60

GAAGAAACTC ATTTGTACCC AATTAAAGAA GGAGATAAGT TTATTGGTAT TTTTTATGGC   120

TACAGAAAAC CAATAAAAAA GCCATTAATA AAGTATCAAA TAAACGGGGC TAGAAAAGCA   180

TATGCATTAG CAAGGGCATA TTATATGGAA TTTAGATTTA AAGCCGGAAG TGTTTTTTGC   240

TATTTTAAAG GGCTaTATCG ATTATTAGAT AAAAAAGAA CAAATAATCA TTACAACAAA   300

GTTTTATTTA GTATGTTTAC GGATTTAGAA CAACAAGTAT ATAAATTTTA TGGGAAAAAA   360

TACCCGGAAC AAGGACCGTT AATAAAATGG ATACTAAAAA ACCTAAAATA ATAACAATAG   420

CGTCAATCAA GGGCGGTGTT GGGAAAAGTA CGAGTTCAAT AATATTTGCG ACATTATTAG   480

CTCAAAAATA TAAAGTATTA TTAATAGACC TAGATACTCA AGCATCTACT ACCAGTTATT   540

TTTGTAAAAA ACTTGAAAAT CAAAAAATTG ATCTTGTCAA TAAAAACATA TACAGAGTAT   600

TaAAAGATAC ATTAGATGTA AATAATGcAA TTGTAAATAT TaAAGAGaAT TTAGaTTTAA   660

TACCAAGTTA CATAACTTTG CATAAATTTT CAAATGAATT TATACCCCAT CAAGAGTTGA   720

GATTAAAAGA TAGTTTAATC TTTTTAAAGC AAGATTATGA TTATATAGTA GTAGATACTA   780

ATCCTAGTTT AGATTTTACT TTATCAAACG CTTTAATAAC TAGCAATTGT GTAATAGTTC   840

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1011

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CAATGACGGC AGAAAAATGG GCAATAGAAA GTTTAGATTT ATTAGAATTT CATATTGAAA        900

ATTTAAAAAT AAAAATACCA ATTTTTCTTC TTGTGACAAG GTTTAAAAAA AACAATACTC        960

ATAAAGAATT ATTAAAATAT GTTGAATCTA GGGAAAGATT TTTGGGATTT ATTCATGAAA       1020

GAGAAGATTT AAACAAAAAA ATTGCGGGCA ATAATGAATT CAATATGGAT AAAGACTATA       1080

TTAATGAATA TAAAGAAGCA TTATCAAAAT TTTTTGAGAT ATATTAAAAA ATTTATTATA       1140

AAAAAAATCC AGATTCTGGA CTTTTTTGAA ATAAAGGAGA TTTTTTATGA AAATAGAATT       1200

AAATAAAAGA ATTTTGGCAT CAGGGATAGA TCCCGATGGT AAAAAGAAG TGATTACCAA        1260

TGAAGATAGA ATTGCTCATT ATAATGCTTT GAAAGATAGA TTAAAGGCTA ATTTTAGAAA       1320

AGAAATATAT CATAAATTGG ATAGCATCAA AATTTTGAAA GAAATAAAGG ATAATCAATA       1380

TTATAAAATT GATGGATATA AAAAATTTGA CTATTTTATA AAAGATTATA AAATAGCTAG       1440

AAGTCAAGCT TATAATTACT TAAAATtTAc AACTGCGTTG CAAGAAGGAA TTCTTAAAGA       1500

AGATTATTTA ATAGAAAATG GCATTCATAA TTCTCTTGAT TTAATAAAGG ATAAAGAAAG       1560

TCCAACATTA AAAAAGTCTA AACAAAATCC AATAAAACCT CTAAGATTTC AACTTAAAAA       1620

TCAAGAAAGT TATGATTTTT ATAAAAGCAA TGCTAAATTT ACGGGATTCT TGTTAGATAA       1680

ATTATTTATG GATAAAAAAG AAATAATTAA AATAATTATG AAAGAATATA AACAATTAAA       1740

GGGATAATAT GGAGGTTGTA TGAACAATTT AGCTAACAGA ACGTTTAACA TAGGAAATAT       1800

AAAAAACGAA TTTTTAGAAA TAGGATTTAG CGAAGAGGcA ATAGATTTTG TTTTTCTTCA       1860

TAATGATAAT TATAACTTTG AGTTTTTAAA AGAGAAATTG ATTAATTTAG AGAAGAATTT       1920

ACAAAAAGAT ATATCTAATT TAGATATCAA AATAAATAAT GTTAAAAACG AACTTAATGC       1980

TAAAATAGAT AGTGTAGAGA AGAATTTACA AAAAGATATA TCTAGTTTAG ATATCAAAAT       2040

AGATAGTGTA GAAAAGAATT TACAAAAGA TATATCTAGT TTAAACACCA AAATAGATAG        2100

TGTAGAAAAG AATTTACAAA AAGATATATC TAGTTTAAAC ACCAAAATAG ATAGCGTAGA       2160

AAAGAGTTTG CAAAAAGATA TATCTAATTT AAACACCAAA ATAGATAGTG TAGAAAAGAG       2220

TTTGAATCAA AAACTTAGCA TGGGTAACAG ACTAGTACAT TTTATGATAA TAACAGCAGC       2280

AATTCTAGGT CCAATTTTAA ATGCCCTATT TATGAGGTAT TTACAATACA TCAAATAATG       2340

ATGTATTGTA TAATTTGATT TTTAAAATGG TACATTATAA TATTGATGAA GAGTATTATT       2400

AATTAACACT TAATTTTTGC TTTTTCATAA AGTAGAACTT ATTTAAATTT TTTAACAAGA       2460

TAACTTAAAT AAGTTCTTTT ATTTTAACAA ATACAAATTG ATTTTAATTC TAAATTGGAC       2520

TATACTCAAT TATTGAAAAG CTTTTTAAAA TTATTTTAAT AAGTGAATTC GGTTAAACCC       2580

TAGCTTTATT AAGTTCTTTA ACAAGAGAAT TTAATAAAGC TTTTATTAAT TATAATAATT       2640
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TCTGTAAAAA GTTGGCAAAA AACAATTTAT AATATTATTA TAAATATTAT AGGAGGGATA   2700

TGTTATTATA AATCCGATTT AGTTTGGGCT TAACTAAGTT CTTTTGTTTG AGAATATAGT   2760

TAAGCTCTTT TTTTTATAAA AATTGTTATA AAAAGTTGGT AAAAATAGTT TTTGTTATAT   2820

ATATGTATGT GAATAGCTAA AAAAGTGTAT TGCTATCAAA ACAATCCAAT TAAGTTGGGT   2880

TTAGCTAAGT TCTTAGACAA GAGAATTTAA ATAAGCCCaA CTATTTTTT TGTAAAGATT   2940

TTTGTAAAAA AgTTGGCAAA AATAGTTTTT GCTATATACn TATATTTATG n   2991

(2) INFORMATION FOR SEQ ID NO: 42:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2988 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTATTTGAAA ATTGCGAGCA TAATATGTGT TTTTTTATTT TAGCACAAGT TTTTTAGACT   60

TTCTAAAAAA GTTAAAAAAA AAGAAGATGC TGAGTAATTT GTATAGTTCT TTTAAGATTT   120

TCATTTAAGT AATAAATTAT ATTATCTTGA TATACTTCTA ATATTTACCC ATCAATAAAG   180

CTAGTGTGGC TTAACAAATA AAAACCAATA AATATTTAAA AAATGATTAA TTTAGAATAT   240

AATTTCTATA GCTAAAGCAA AAAATAAATA TAAATTTGGA CTAGTTTTAT TACATAAAAA   300

GATAAAATTA GTCATGCTTG TTGCAATAGA GCCTACTATC TATCCCGCGA GGTATATTTA   360

TTTATATTGC TTTTTAGTTT TTGTAAAGTG ACTTTTAATT ATTAAAATCT AAGGAGAAGA   420

GATTTATGAA CAAAAAATTT TCTATTTCAT TATTATCTAC AATATTAGCC TTCTTGTTAG   480

TATTAGGTTG TGATTTGTCA AGCAATAATG CTGAAAACAA AATGGATGAT ATTTTTAATT   540

TAGAAAAGAA ATACATGGAT AATTCAAATT ATAAATGTTT AAGTAAAAAT GAGGCTATAG   600

TTAAAAATTC TAAAATTAAA TTAGGTGTAA ATAATACTAG AAGTCGTTCT TATTCTTCTA   660

GAGAGACTAA TGTTTCGGAT TCCTATAATA AAACCTATTC ATATTGCAAA AGCAACTGAT   720

TAATTTTATT ACAAAAAAAC AAGAGAATGC TCAACCCATA ATTAGGTGAC AATTAATTGA   780

ATATATGCAG GGATTATTAA AAGTTAGCTT CTGTGACATT ATACACTTGA ATATAATATT   840

ATAAAATAAT AGAATATATG GGTGTTAATA AAGCTTATAA GCATAGAATA TATCATATAA   900

AGAAGAATTT CTATCCCCTT AAAGGAAGTT GATAGTTTAG CTCTTTGTAA TGTCCAACTT   960

GACTTAGACT CTGCGTATAA TGATTTTTTT AGAAAAATTT AAAAGGGAAA TAGAACACAA   1020

1013

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GGATTTCCTA AATATAAAAG TAAGAAAAAT AGGGAAACTT ATAGAACTAA TAATCAAAAA        1080

AACTCAATAG GAATAAAAAA TGGTTATATA AAGCTACCTA AAATAGAGTT TATAAAGTTA        1140

TGTCTATAAA TATTATATTT CAATAACAGT TGAGTGCTTA GATACTAAAA ATAATAATGA        1200

AACTAAAGGT GATAAAAAAG AGGCAGTTGG TATTGATATG AGCATGAAAC ATTTTTTAGT        1260

AAGTAGTGAA GGTGAGAAGA TTAATCATCC TAAATATTTA TTAAAAAATG AAAATAAACT        1320

TAAAAAATAC CAAAGAAAAC TATCAAAAAA GCAAAAGGT TCTATTAATA GAGATAAGTC         1380

TTAAGGTTTA GACTTGCATT TATATCTCCA TCATGCAAAG TTGTTACAAC TACTGAAAGC        1440

CCACCTAGTA TCACTTAATT TTAGAGCCAT ATTTTTAATA TGACAACTAC TACATACATA        1500

TAAATCAAAA TGGTATGGAT CTGCTTTGTA TAAAGTAGAT AGATATTTTC CATCAAGTAA        1560

ACTATGTAAA TTGTCTTGCA AACTCAGACC ATCCTAAATC ATTAATACTT TTTCCAAACA        1620

TTCCTTTTCG CATGCCTTTT TTCATTCTTA GAATTCGAAC TGTAATCAGA CCTTTATATT        1680

CTTTATCAAT TATCATATTT TAGATTTAAA TTGTATATAG CAAAAAGGTC CTATATGGGC        1740

TATTCCGTTT GCAGTAAATA AATAGGGATT GGAATTAAAT CCCTAACCTA ATTGAATAAT        1800

ATCATACTTT CTTCAAGAGG ATTCCCTTCG GCCACTTTTT TTCTTCGTTC TTCCATTACT        1860

TTTTTATATT TTTCAGCTTG TTCTCTTCTT TTTTTATTTA ATTCTGTCGA TTCTCTTTTC        1920

TCTTTTTATA ATTTTTCTTG AACTACTAGT GGCTTAACTG TTTAGATTTG GGATCGTCCT        1980

AGTTATAATT TTGGTACTTC TAATTTTTCT GCTACCACCT TTAATTCTGC CTCTAGATTT        2040

GCTCAAATTT TAGGGATTGA TTCTAATTCA TCTCCTTTTA AAGATTTTTT TCTTCTACTT        2100

TCTTTCCCTT ATGTGCTTTT AAATCAAATC TTTTTGAATT ATCCATAGCT TCTGTTGCTT        2160

TTCATATACT GTTGTATAAT CTAGTGTCAT TTTATTTGGA TCCATTTTAT TTTTAGATGA        2220

TAACTTTTCT AACTTTTTTT ATTATCTTTA TCTTCTTTTT TTAAATCACA CGAAAATAGT        2280

AAAAATAATA GCAAGTAATG GCTAGGCATA TACTTATCTA ATTTAGAGAT TAGCTCCTAT        2340

ATTCAAGCGG CTATTATCCT TATTCTTCTG GCATAGAAGT TGAAAATTTA AATTTTAATA        2400

AATTGTATTT TTATTTTAAT GAGAATAAGC AGAAACATTC CATTCTTAAT TGAATTCATT        2460

AGAAAGTTTC CTTCTATTGC TAATATCATT AATATAATAA AATAATTATC AAAAACATTA        2520

GCAAATCCCC CTTTATCTCT ATGATACTCC TTCACATCTA TATGATTTCT ATCTTTACTT        2580

TCTACATTAG GCTGATTATC TCTACCATAT TTAATATAGC TAAGCGGCTT TTTAACTTTA        2640

CCCATATTTT TCAGTTTGAA TAAAAACCTT TTAACATACT CTTCTATTTG GGATACATCT        2700

CCTTTTCAAT AAAAATTAAA ATGCGCTGAT TTTAATACAT TTACGAAAAA AGTTAATGTA        2760

TCGAGTTTTT CATTACTAAA TCTAAGATTG CTTTTCTAAC TCAGTTTTAA ATTAATACTT        2820
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TCATAAGCTT TACAAGCTTT AGTCACTCCT CATATAAAAT CCAAAATTCA ATTGTTTTAT   2880

ATAAGTAAGT ATCAAGTAAA TTTAAATTGG ATAGTAAAAT ATTAAATAGG GGAAAAAACA   2940

AGCTTAATAT TGAGTGATAA ATAAATTTTT CTCTTATTAA ATAGTATA   2988

(2) INFORMATION FOR SEQ ID NO: 43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2970 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGAGTTTTTT CGTTCTTTAA AGTACTTGTT GATTTCTGG TAACATTCTT TTTTAGGATA   60

CTTTAGCTTA TAGTAAATTT CAGTtCCACA ATTTACACCC ATGTGTTGGT AGTAATTCGT   120

TGTGACTTTT AATACTTTTT CTAATTTATA AAGATAATTT TgCaTTGTTC TCAGTGTAGT   180

GGGAGCCAAA CCATTTCTTT TTAGATTTTT ATTATAGTAA TAGAGTATGT TTTGTTGTGT   240

ATATTTCTTA TCTTTTTTGT TTAGAAAATC TACTGTTGAT GTAAGATATA TTAACTTGTG   300

TTGGTGTTTG TTGTGGCAAG TGGGATTTTT TGTGGTGATT AAAAAATCTT TCATTTTTA   360

CTCCTTATTT TGTTATTAAC AATTACTATT ATAATGCAAA ATTTTGATTT AAAAGTAAAT   420

ACTTTTCTAA AAAAATATTA AATTTTAATT ATTAATCTTA TTAATTAAAT ACACTTTTTG   480

TAATTTGGTA AAAAGATTTA TTGATTTTAA TCACAAATTA GACTATACTG CAAATAGCGT   540

AGGAAAATAT CTTCATATTT TTACCTACCT TATTTTGTAG TTTTCTAAAA TCATAGTGGG   600

AACTTGGCGA AATTCTTTTT AAAGGGAATT TGGTTAAGTC CCACTTCTTT TGTGTAAAAT   660

TTTTTGTAAA AAAGTTGGCA AAAATAGTTT TTGCTATATA ATTATTTATT ACAAAATAAG   720

GAGGAAAAAG ATGGAAAATC TTTCAAACAA TAATAATCCA CAAGAAAATA TTCAAGGAGA   780

AATTAAATTC AGAAAGATA TGAGCACCCT AATCAGAAAC TTGCCGCGTA TTGACAAAAG   840

TCTTAAAGGG TATGGGTATA AGTATCAAGA TTTCAATGAC ATAGTAGAAG TAATTTATAG   900

TGTTATTGAT AAGCATAATT TGGATCTTTT TTTTACGCAA GCCCCAATTT CTGTAGAGGG   960

GCAATATGGC ATAGTTGATT ATATTAGGAC TACATTCTAC AGTACAAGCA CTGTGTACAA   1020

ATACTCATTT GATACGCGAA TTCATACAGA TAAATTACAA TGGAACAGTG AAAATGGGTC   1080

TAAAAATATG AATACGATGC CACAATTTGT TGGATCAGCT ATTACTTATT TCAAAAGGTA   1140

CGCTTTAGTA GGGCATCTTT GCATAAGAAG CGAAATGGAT ACTGATGCAG CACCTATTTA   1200

1015

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CAATAATTAT GAAAACAGAA ATTCTATGCC TAGCAAACAA TCTAGTGTTA ATCAAAAGCA     1260

AGAACAAAAA AGAGAGCAAA AACAAGAGAT TAATCAAAAT CAAAAAAATA ACACTATTCA     1320

AAACCAGAAA AGAGACATTA AGCAAGAACA AAAAAAAGAT AGGTTTTATT ATTACGGTGT     1380

TTTTAAAGAA GCGTTGTCTA ATATAAAAGA TTGGGTAAAT AGCCCTACAA TAAAAGATAA     1440

TATAAACTCA ATTATTCAAA AAATAAGCTT TATTCAGAAT ATAGACCCCA ATAATGTTGA     1500

TGATATCAAG AAAATTGAAT CTGATTTAAT CTCGTATTTT GAGAAAAATA GTGATTTTAA     1560

AAGTATAAAC TATTGGGCGG AGATTATAAA AAACTATTTC AAGAAAAATA ATAGATTAAA     1620

GGATTTACAA GATTTTGAAA AGTTTGTGTC GTTAAGAGG ACTGCTTATG GCCCTAGTCC      1680

ATTAATATTC TTTAGTGTCT TAAAAGAATA TGAACGGTTT GATTGCATAT TTGCAGCATA     1740

GCGAATTCTT ATATGGTGAA GCCCCCACAT GGGGGCTGCG ATATTATTGC TGAGCTTGGC     1800

AGGTACTACT TGCACTAGTT GCAAAACTAT CTATACCGCC ACCAAGAGCC CCCTTAACCA     1860

CCTCTTTGAA GGTGCTTTTT TGTTGTTCAG AATTATCCCC AGTACACTTA TCAAGTTCAC     1920

TCTTTATATG ATTAAGTGCA CCTTTTATTT TGTCTTCGTC ATATCCTAAA AATTTATCAA     1980

ATTCTCCAGC ACCAGTTAAA GCGGTTTTTA ACCAGTCAAG ATGTGTTTTT TGGTCTTCAG     2040

ATAGCTTTTC TCTAAGCAGG TCTTCTTTAG ATTTTGGTTT TTCTTGTGTT GCTTCTTTTT     2100

GGGTTAAATC ACGTTTTTGT CTACTTTTTG TTTGGCTAGT ATTAGTATCA TTAGAATTAC     2160

AGCTGTTTAG CATTAGTAAA AATAAACAAA ATAATATGTT GATAATTTTC ATTrTTATTC     2220

CTTTTTTTAT TATTAATATT CACTTAATCA ATTATTAATA CTAAATATTG GATAAACAAT     2280

TATTATTTGA ATTGATATTC TTTAAGTGAG GTAGTAGCTA TTTAGAAATG AAAGCAAATA     2340

TTAGCCCGGC TATCATTGTT ATAGACATTG CTCCCATAAT TCCTAATACC CATTTAAGCA     2400

TTTCTGAAAG AGACATTAAA TTCTTTTCCA CATTGTCTAT TTTAGCAGTA AGTTCATTTT     2460

TAACACTATC TATTTTTAAA TTTAAATTCT TTTCTACAGT ATCTATCTTA GTATCTAAAC     2520

TATCTATTTT TAGATTTAAA TTCTTTTCCA CATTGTCAAT CTTAGTATTA AGTTCGCTTT     2580

TAACAGCATC AATCTTAACA TTTAAATTCT TTTCTACAGT ATCTATTTTA GAAATAAGAT     2640

TATCAAATTT TATATCAAAT TGTTTTTCTA AATTTTCTAA ATCTCTATAT GTTAGTTCAT     2700

TGTGATAATA TCTTTTAGAT AAATCTTGTG CTATTAGTTG TTCCATGCCC AGTCTAATAA     2760

ATTCTTTATA TATTTGTTCT TGAGTTACAC CTGCAATATT TGTTGACACT GTTTCCATAA     2820

AATTTTCCCT TATGGTCATA TTATACACTA TTTTAGATTA ATTGGCTTTA GAGATTTTTA     2880

TATGTAAAAT AGAATTTCTT GCAAGAAAAA CCTTTTTGTA ATTTACATTT TTAATTGGGA     2940

ATATTTATTA TAGACTTTTT CCGCTATTGG                                     2970
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(2) INFORMATION FOR SEQ ID NO: 44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2942 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

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AGAATAGCTT GAAGTAAGGA TAAATGAAGT AGAAAATTTT GCCTGCTTAG TGCAAATTTG      60

TCTATTCCTA ATAGCAATAA CACTTCTGAA TGGAGTTTTG TTACTAAAAG TTCTTCTTCT     120

CCCGCAACTT GTGCTTGTAA GCTTTCTTGT TCACTCATTT TCACTTACCT TATACTTTTA     180

ACTTTGCTTT ATGTTAACTT GCAAAATAGT TTTTCTAGTA GCAAGTAGAC CGCCTAAAAC     240

AAAATCAATG TATGAATGAG CTACATCGGT TGAGTCTTTA TCAACTTGTT CATTCGGTGT     300

AGGTAGCATA TACTTACTAG GTTTAAATTT AATAAGTTCT GAATTGAGTG GATAAATGAG     360

TATTTTATGT TTTAGCAAGT TTGAAGTTTC AATGTAAACA TCTTCTCTAT TATTAATAGC     420

CTTAATAGTT TGAATTAAAA CATCTTCCCA TTTTTCACAA CTACTTGCTG CACCCTGTGC     480

TGCTGCGTAT GGTTTTACTA GTTTAAGTGA CGTTGCTGGG TCAACTATTA CCATCATCGG     540

TGTGGAAAAT TCGTCGCCCA GTTCCAACTT TGAAAGTCCA GCCTCAATTT TTTCAAATAT     600

TTTATCCATT TTATCTTTAT CACCACTAGC AACCTCTTCT TTTATCTGCT CGGGCATATT     660

AAGCAGCCCA TACATATTTG GAAGCAGGCG TTTTTGATTT TTTCCATCTT TTTGAATCGA     720

AACAGTTCCT GTTAGTACAA AGTGATTAAT AAGTTTAATA ATTTCACTAC TTGCAAGCTT     780

ATACGCTTGA GCAAAAGGAA GTAAATTATT ATTAATGTCC CCAATATATG AATCTGAAGT     840

ATAAAATTTC TCAGAAGTCT GCTTTAAATG TCTGAATTTA TACTGTAATT TCAAATAATT     900

AAGTCTTACC ACTTCAGAAC TAAATCCAAT AGTTGAGATA GTATTAACCT CATTGGCAAT     960

TGTTGTAGGA TTAGCATTTA AAAACGCGTC CCATTTTACG GTTTTTTGAT ATCCCATTTG    1020

TAGATCAACA TCTTCAATTT GATCGGGCGA AAACCATTTA TACATAATAG GATCTTTAAC    1080

TTCTCCTATG ATATTTGCCA CAGCTTTTGC ATAATAATTT TCATCAAATA ATTCCATATT    1140

AAATCCTCCT AAATATTATT AATTTCTACT CATAGCTTTA TTCCCAAATA CAGCTACTTT    1200

TACTAAATAA ACCTCATTGC TAATTTGTTT CGCATCAGTC AATGCTGTTG CATTAATAGT    1260

TGCTTTATTT GGTGCTCCAG TCACCTTTTC AAGAGCACCG TCTTTATTAA AAACAAGTTT    1320

GTCTTTTACT TTAACCGTAG AATCTTTTGC CACTAAATAT CCCTCAAAAT TATTGGTAAT    1380
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TGGCACAATA GTAGCTGTTT TACTAAACTC ATCTATGTCA ATGCATATTC CATATAAGTC   1440

TTCACCTCCA CCAGCCTCAA CATGTGGCTC ATAGTGACTT TGATTATCTT GAGCCTCTTG   1500

AATAACTCTT TTTACTCCAC GCTTGTACGG ATACCCCAAA AATGGATGAT TTTCCAATTT   1560

ATCAAACTTA CTAGTTCTAG TGCCTCCAGA AGCAAAAAAT TtCaCATTTT TGTCTCTAAA   1620

TTCATTAGAA TTGCTAAGCA AACTAGCGTC ATGTTGGGGA TTTTtCATAA ACTTTTCCAG   1680

TTTACTTCTT TtCTCTkGAT ACTCTTTTAC TAATTGCGTT GTATCTCCCA TTTATTTACC   1740

TCCTTTTATT CGCCCAAAGT TTAACCACCA TCAGGTATTA CTATCTTCTC AAGGCCTCTA   1800

TTTCCAAAAA TTGCAACTTT TATCAAATTA ATAGAATACT CTTGCCTAGG ATATCTATTT   1860

TGATCTtGAT TTCCAtCTTC GGGTGCAAAA TTGATtGTAA ATGAATCAGA TAGAGCATAT   1920

ATGTTAATTA CGGTTGGTGG CCCACCTCCA GCCTTGATAA TAACACCGTT ATTATTTATG   1980

TCTAGGATTT CTCCTATTTT TATACTTGGA TTCCTTGTGA CAAGGTACCC TTCAAAATTG   2040

TTAGTAATTG GCAATACATA CGCGGTACAA CTAAACTCAC ATACATCTAC ACATATCCCA   2100

TACATATCAG TATCAGCTCC AACTTCyACA TATATAGAGT CTCTTTTGG AACAAGTTTA   2160

ACCCCACGCT TGTATGGAAA ACTATTTGCT GGGTCGTAAA GGTATTCCTC TATTTTGTCT   2220

GTATAACTTG AACATGCAAA TGAATATGCA TCAACTCGCT CATTCTTAGA TTTAAAACAA   2280

CTACTCAAAC CGCCAAAAAC CTTATTTTCA ATTGAACTCA TAGATTTTAC ATATTTCTTG   2340

AATTTCAAAA GGATATCATC AAGCTCGTTA ATTGCCTCCA AATAGGGATC TTCCCCTTGT   2400

GCATCCTCAG CTTGTCTTGC TTGCCGTTTA GCTCTAGGAG CAGCGGAAAC TTGTGCCCCT   2460

AAATCTACCT GTGGGTCCTC AACAGCCTCA AGATTTTCTA CTTGCATGTT GCCTTTTAAA   2520

GCCATAATTT ATTACCCTTT TATTGCTCTA TTCCCAAATA CACTAGCAAG CACTATAAAT   2580

AAATCTTCAG TTAATTTGTG TGCCTTTGAA AGTGCTATTG CATTAACAGA TTTTTGAGCC   2640

CCAGTGACCT TTTCAAGTTC CCCATGTTGG TTAAAATTTA ATTTATCTCC TGGATTTACA   2700

CCATTTTGTC CTTCTTTCTT AAGCGTTAAA TACCCAGTAA AGTTATTTGT AATTGGTATA   2760

ACAGTTGCCA TACCGCTAAA CTCATCTATA TCGGAACACA CTCCATATAA ATCGTCTCCA   2820

CCACCAGCCT CAACTTCTAG TTCGGTTGTT CCATCTCCAA AACTAAGCTT AACACCCCGT   2880

TTATACGGAT ACCCTTTAGC AGGGTAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC   2940

CC   2942

(2) INFORMATION FOR SEQ ID NO: 45:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2892 base pairs
      (B) TYPE: nucleic acid

1018

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

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GGGTCTATAA TGTCATTTAT TATTTCCTCA GTGCTTTTTC CAGTTTTTAT TCCGTATTCT      60

TGCGCTGCTT TATAAGAGCT ATACATTTGA CTTTTTTGTT CTTGCGTTGC TTGTTCGGTT     120

TCATAAAGTT TATTTATTGA CTTTTTTAAA TCTTCACTAA GATTATCATA AAAATTTGAA     180

ATTTCATTAG TATGCATATT AATTATAGAT AGTATATAAA TAAACAATAT TTTGAGCAAT     240

AGTTTTTGGC ATTTTTTAAA TGAAAGTTTT GATAGAAAC ATTTCTATAT TCATAACAAT     300

GAAATCTACA AAAAAATAAC AGCCAGTGAA CTTTTCTACT AGCTGTTACT TTGTATACGC     360

AAATTTAGTT ACACCTAAAA GCATCCAATA TAATTACTGA CTGTCACTGA TGTATCCTTT     420

AATTTCTTCA AATTTAGAAC TATCTTTAAG ATATTTTTTA ACTTCTTCTA ATTTTGATTT     480

TAATTTTTCT AAATCTTCTT TAATTTCGCT AACATTTACA CTTTCTTTTA ACTTAGGCTC     540

TTCGTAACCA GTATATGGTT TATTGCCTTC ATTTAATTTA GTTCTTAGCG CGTCCCTAGC     600

ATCACTCAAT TCTTTCAATA ATTTTCCTAA TCCTTCGTCT TCTGATTCCT CTTCTAACCC     660

CTCCCAAGTT TCGCGTATAG AATTATTGCC ATTGGTAAAA TCATCATACA CAGGCCCAGT     720

AATTCTATCT ATAACGCCTT GTGGGCCTAC AGTCGTTTGC CATTTTATAA CATCAATATT     780

TTCATTGAtC TCATCTATTT TAGCTATAAG TGTTTTAATT TGGTTATCAA CTTGCCTTTT     840

TTCTTCCTCT TCTTGTTGTC GTTTTTGTTG TTCTGCCTCT TCTCTTTCTC TTTTTTCTTT     900

TTCTGCTTTA GCTTTTCTTT GTTGCTCTTC TTGATGTCTT TTTTGTTCTT TTTGTTGTTC     960

TTCTTCTTTA GCTTTAGCTA ATTCTTGTTT GTTTTGTTCG TCTATTATTT CTTTTTCTTT    1020

AATGTTTTCT TCTGTATTCT CTTGTTTTTC TTTATTTTCT TCAACTTTAG CTTCAGCTTC    1080

TTCTACTTTT TTTTCTTGTT GACCATCACT TTGTTCTATT GCTTTTAATA CTAATGCATT    1140

ATTGTGAATA TTTTCCGGCA ATACTGGTGG CGGATTTATT CCACTGCCAT TAGGATCATC    1200

GCCCTGCATT AATTCTTCTT TTTCTTCTTC TTGTAATTTT TTTGCTACTT CATCTACTTT    1260

TGTACCACTT GAAGCAATTT TATCCTTTAC TGGATCTAAA ATCTTATTTA CAAATCCTTT    1320

AATTTTCCCT TCTGAATTTT GTTTTATATC TTTACCAGTT GCAAAATTCT TGCAAGAAAT    1380

TATCAGCGCA AAAACAGCAC AAATAATCAA TGTTTTTTTA TTCATAATTA TTCTCTCCTA    1440

TATTTCTAAA TTCTATTTTA AATTTTTTTT AAGCACTTCT AGTGGTATTG CATATTCAGC    1500

TGTTTTATCT CCCCCCACAC CGTTATTAAT TTTATCTCCT AAAAACGCAA TATGTTCAGC    1560
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ACCATTAATA CTTTCTATTT TTGTTATGAT CTCTTTGTTT TGGATACCAT TTGCACTACT   1620

TTGTTCGTAC TTATATCCAT AATACAAACT AGTTTTAAAT GATCCGCCTT TAGTCATTGC   1680

TTTTATAAAG TTATTAACTT CTGATTCTTT TAATGAAAAG AATGTAGCCG AATGTCCCCC   1740

AGCGTTTAAA CCCGTATCAA TACCATTTTC TTCTTTTCTT ACAACTAAAT CTCCTAGGTC   1800

TGTCCAGTTA CTATTATTAT CTTTATTTTT AATTTTTACA GTAAATTTAG AGAATTCTAT   1860

TTTTTTAAGT TTTAACTCAC CATTACTTTG CTCATCATAT AAAGTATGGT TTATCTCACC   1920

ACTACTTTGC TCATCATATG AAGTATGAAT TTTGCAAGCA CCTATAAGTA TAAAAACAGC   1980

ACAAACAATA AACATTTTCA TTTTCTTATT CATAAATTTC TCCATAAGTC CTAATCATAC   2040

CACAACAGCT AATAATTGCA ATATTTCAAA GATTTAAATA TATAATTTTG TTACATTCAG   2100

CTATTACATA TTAACAAAAC TCAAATGTAA TTTTAACCAA CTCCCAAAAA TCTCTCCATT   2160

GCAAATGCCC GGCTCATTAC AAAAGACTAC AAAACACATA CAAATTAAAT TTCAAAGTCT   2220

TTGCTATATA TCACTTAAAG TATCATGTCT TTCTTAAGTC CACCCCTTAA AAATTGCCTC   2280

TTCTGTTTAT CACAGCCACT CCACAACCCA AATTTCGCAT GCAATGAGAA CACCATAAAT   2340

TTGACTAAAA TTTTAGGGTT TTGATAAAAT ATAAATTACA TTTTTATTAA ATTTTTATTA   2400

CTTTTACTTA ATTTAAAAGT AACACTTCAA AGGAGAGGAT TTTATGGATA CTAATAATTA   2460

TTTTAATTTA AATAATTTCG ATACAGATTT GATGCACAAA TTCTTAAAAG ACTATCAAAA   2520

TGTATTAAAT GAAAACAAAA TTCTTAAAAA TTCACTAAAA ATTTCTTCTA AGCCTACTAA   2580

AAAAGCTTCA AAACCAACTC CAAAGTTTTA TTTGAATCAA AAAATTATCA AAATAATTGA   2640

AAAATGTGTT AAAACATTAA AATAAATTGA CCCAATTTCT GGTTGGTTTT TAAATCTACT   2700

GGCAATAAGT GGCTGCAGAG GTGCCGAGCT GCAAAAGTA AAAATGCAAG ATATTACTCC   2760

CTTTTTAAGC AAAACTGGAG AAACTTTTTA CAATATAAAA GTAAATGTAG CTAAAAAAAG   2820

AAATGTCACT TGCATTAGAG AAATTGTCAT AAAATCTGTA GAATTTGATG CTATTCAAAA   2880

AGCTCACGAA AA   2892

(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2849 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTAGAAAAG CATATGCATT AGCAAGGGCA TATTATATGG AATTTAGATT TAAAGCCGGA   60

1020

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AGTGTTTTTT GCTATTTTAA AGGGCTATAT CGTTTATTGG ATAAAAAAAG AACAAATAAT      120

CATTACAACA AAGTTTTATT TAGTATGTTT ACGGATTTAG AACAACAAGT ATATAAATTT      180

TATGGGAAAA AATACCCGGA ACAAGGACCG TTAATAAAAT GGATAATAAA AAACCTAAAA      240

TAATAACAAT AGCGTCAtTA AGGGCGGTGT TGGCAAAgCA CAAGTGCAAT TATATTTACA      300

ACTCTATTGT CTCAaGATtG GAAAGTGCTT TtAATTGATA TGGATACACA GGCATCAGTA      360

ACTAGTTATT TTTACAAAAA AATAATAGAA GATAATTTTA ATTTATTGGA AAAAAATATA      420

TATGAAGTTT TGAAGGGGAA TGTATTAATT GATAATTCAG TTATAAATAT TAGTAATAAT      480

TTAGACTTGA TACCTAGTTA TATAAGTTTA CACAAATTTA ATAAAGAGGC TATAACATTT      540

AAGGAAATTA AACTTCAAAA ACAGCTATTA AATTTACAAT CCAATTATGA TTACATAATA      600

ATTGATACAA ATCCCAGCCT AGATTATACG CTAACCAATG CTTTAGTATG TAGTGATTAT      660

ATAATAGTTC CAATAACAGC AGAGAAATGG GCTGTTGAAA GTTTAGAACT TTTAAAGTTC      720

TCAATTAGTG ATTTAGCCAT TGATATTCCA ATTTTTTTAA TAATAACTAG ATTTAAAAAA      780

AATAATACCC ATAAGGCACT ATTTAGTTCG CTTAAAGACA ATAAGAATTT TTTGGGGTTA      840

ATTTATGAAA GAGAAGATTT AAATAAAAAG ATAGCAAAAA ATGATCTATT TAATTTAAAT      900

AGAGATTATA TGCTAGAGTA CAAAAATATA TTAAGTAAAT TTATAACAAT AATCATGTCC      960

AGGTAACTGG ACATGATTGC CATTTTAAAT GAAAGGAGTC CATATATGGA GATAATATTG      1020

AACAAAGAA ACCTAGAAGT GCTAAATGAA GCCGAAGAAC ATTACAAGAA GTTAAaGCAA      1080

AGATTAAAAT CTAGTTTTCA ACAAGAAATT TATTATAAGA TGGAAGTTAT TAAGATATTA      1140

AAAGAAATAA AAGATAACGA ATATTATAAA TTAGATGGAT ACAGAACATT TGAAGATTTT      1200

ATCAAAGATT ATCATTTAGC AAGGAGTCAA GCATATGACT ATTTGAAAAT AGCAAATGCA      1260

ATTAAAGATG GCATTTTAGA AGAAGCTTAT GTAATAGAAA ATGGTGTTAC AAAAACTCTT      1320

GAGTTCTTAA GAAAATCGCC AAATGTTTTG AAAAAATCTA AACAAAATCC AATAAAACCC      1380

TTAAGATTTC AACTTAAGAG TCAAGAAAGT TACGACTTTT ATAAAAGTAA TGCTAAATTT      1440

ACTGGATATC TTTTAGACAA ATTATTTAAT AATGAAAGG AAATGATTAA AAAAATTATG      1500

AAGGAATATA AACAACTGAa AGGATaGTAA GAAGTTTTAT GACTAATTTA GCGTACAGAA      1560

CATATAACAT AGAAAGCATA AAAAATGAAT TTTTAAACAT AGGGTTTAGT GAGGAGGCAA      1620

TAGATTTTGT TTTTCTTCAT AATGATAATT TCAATTTTGA ATTTTTAArA GAGAAAATAA      1680

TCGATTTAGA AAAGAATTTG AGAAAGATA TATCTAATTT AGATATAAAA ATAGATACTG      1740

TAGAAAAAAG TTTAAATCTA AAAATArATA CTATAGAAAA AAGTTTAAAT CTAAAAATAG      1800
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ATTTTGTAGA AAAGAGTTTA AATGCCAAAA TAGATAGTTT AGATACCAAG ATAAATAATG 1860

TAGAAAAAAC TTTACAAAAA GATATATCCA GTTTAGATAC TAAAATAGAT AGTGTAAAAA 1920

ACGAACTTAA TTCTAAAATA GATAGTATAG AAAAAACCTT GCAAAAGGAT ATATCTAGTC 1980

TAGATAATAA AATAGATGTT TTAAAAAATG AACTTAATGC AAGCAATAGA ACAATACAAG 2040

TAATTCTAAT AATGGGAATA ACACTtGCTC CAATTATCTA TTCTATATTT AATAAGTATT 2100

TCTTTAATTG AGAATGATTA AAATTTTTTA AAATATTAAG GGAGTATATA GCGTATTTTT 2160

TAAATAGAAT ACTATAATCT TGATTTAAAT TCTTTAAAgA AACATTTTAT TTTTACTTTC 2220

TTTTAAATTT AGAACTTATT TGAATTTTTT AACAAGAAAA TCTAAATAAG TTCTTTTATT 2280

TTAACAAATA CAAATTGATT TTAATTCTAA ATTAAACTAT ATTCAATTGT TGAAAAGCGT 2340

TTATTTATTA TAATAATTTC TGTAAAAAGC CTGACAAAAA TAGTTTTTGT TATATATATG 2400

TATGTGTATA GCTAAATAAG TATATTGCTA TCAAAAAAAT CCAATTAAGT TGGGTTTAGC 2460

TAAGTTCTCT AACAAGAGAA TTTAAATAAG CCCAACTAAT TTTTTGTAAA ATTTTTTGTA 2520

AAAAAGTTGG CAAAAATAGT TTTTGCTATA TACTTATATT TATTACTATA AAAGGAGTAA 2580

AAAGATGGAA AATCTTTCAA ACAATAATAA TCCACAAGAA AATATTCAAG GAGAGCTCAA 2640

AATGATAAGT ATTAATCAAC AAAGTTTTAC TGGTTGTGAA ATATTTGAGG AAAAATCTTC 2700

TCCCATTrAA GAAAAAGTA AATTAAGTAA GATAGGCAAG AAATTGCCAG GaATAAGTAG 2760

TCAAGAATGT TTTAGATTTA ATCGCAATAT TGATTTTAGT GTGCAAAGAA ACAAGTTAGA 2820

TAAATACGGT GCTAGTGAAG TAGGCAATA 2849

(2) INFORMATION FOR SEQ ID NO: 47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2682 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AGTTGCGTAT CTTGACATAA AAAGTGAATT TGATACTGAT GCAGCACCTA TTTACAATAA 60

TCACGAAAAC GAAAATTCTA TGTCTAACAA GCAAGTTAGT GTTAATCAAA AACAAGAACA 120

AAAAAAGGAC ATAAATCAAG AAAAAAAATCA ACTGAACACC TTTAATAAAA ACTTAAAATC 180

TGGCAAGGCT TATTGCTATG AAATTTTTAG AGACGCACTG TTTAATATAA AAAATTGGGT 240

AAATGAAGGT GAAGAAAAAA ATAATATAAA TGCTCTTATT CGGGCATTAT GTACTGATAA 300

TGATGATGCT TTAGAAGATC TTTTTGAAAA GAATGCTGAG CTTAAGAGTA TAGAATATTG 360

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GGTAAATTTT TTAAAAAAAT ATTTCAATAA AACTAATAGA TTTGATGATC TAAATAAGCT    420

TAAAGTATTT ATGTCTGATA ATCGGGATGT TTATAAAACA AAAGTATTAA AATTCTTTTG    480

TATGTTGAAA AAAGAAAGAC AATTTAATTA TATATTTGCA GCATAGCAAT ATTAAAGCCC    540

CCTATTTGGG GGCTGCTATA GGTATAATAA TTAAGGTTTT TATTTTTGAT TGAGAAATGT    600

TTTTAGTTTT GCCAATTAGC TGTAAGACCA GCATAATGAT TATCTTCTTT TAAAAgTTCA    660

yCTTTAAgGT ACtGATAAAT TTCTTCATTA GAATTCTAT TAGaCATATC ATTAGCGACG    720

CCTCTAAAAT aTTGCyCTAy TAAGTTGTCC ACCTCCCCAT ATTTCATTAT TTTTATTACA    780

ATCTTGTGGA GTGTTTTTTT TACAATCAAT AGCTCCTTTA ATATAAGTAT CAAAAGTTTC    840

ATTTTGTGCT TTTGATTTTA AGAAGTTGTA AACCTTGGTA AAAGCACCAG CTAATTCTTT    900

TTGTTTTTGA ATATCTTCAG AAAGCCAATC AAAGAAGTCA TTACATTTAC TTTTGTTTCC    960

ATTCATGCAC CCTTGTATTT CATTGTTTAA TTTTTCAATT GTGTATTTAA ACACATTGAT   1020

TAATGAAGTA AACATTTTTT CTTCGTCGGA TGTTAAAGTG ATTTTTTCTT GTTGTGGCAG   1080

TTCTTCTTGG CTTAAATCAC GTTTTTTCCT GCTTTTTGTT TGTTGGGCAT TGTTTTTTAA   1140

AGTGTCATTA TCATTGGAAT TACAGCTATT TAGTAGTAGC AAAGATATAC AAAATAATAT   1200

GTTGATGATT TTCATTGTTA CTCCTTTTTT TATTATTAAT ATTCACTTAA TCAATTATTA   1260

ATACTAAATA TGGGATAAAC AATTATTATT TGAATTGATA TGTTTTAAGT GAGGTAGTAG   1320

CTATTTAGAA ATGAAAGCAA ATATTAGCCC GGCTATCATT GTGATAGACA TTGCTCCCAT   1380

GATTCCTAAT ACCCATTTAA GCATTCTGT AAGAGACATT AAATTCTTTT CTACATTATC   1440

TATTTTAGCA TCTAAATTAG ATATGTCTTT TTGTAAATTC TTTTCTACAT TGTCTATTTT   1500

AGTATTAAGT TCGCTTTTAA CAGTATCAAT CTTAACATTT AAATTCTTCT CTACAkTATC   1560

AATCTTAGTA TCTAAATTAG ATATATCyTT TTGTAAATTC TTTTCTACAk TATCwATCTT   1620

AGTATCTAAA yTAgaTmTAT cTTTTwGtaA ATTCTTTTCy ACATTrTCTA TCTTGGTATT   1680

AAGTTCACTT TTAACAGCAT CAATCTTAAC ATTTAAATTC TTTTCTACAG TATCTATTTT   1740

AGAAACAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA   1800

TGTTAGTTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAATT GTTCCATGCC   1860

CAGTCTAATA AATTCTTTAT ATATTTGTTC TTGAGTTACA CTTGCAATAT TTGTTGACAC   1920

TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT   1980

AGAGATTTTT ATATGTAAAG TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTTACATT   2040

TTTAACTTCA GATATCAGTT TTAAATTTTT TACTGTAGAT TTTTTACAAA AACAGTATTG   2100
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CAAAAACTCT TAGATTACTT TTTCTTTTCT TTGTATACTA CAATAACTCC AAAACCCACT   2160

AAATGGTTTA GTGATTTAAC CTCAAGAATA TTTTCGGCAC CTATTTGGTT AATAAAATTT   2220

TCTAACCCTA TCCCTATAAT TTCGAATAGA GTTTTGTTTT TATCTTCTTT TTTTATAGGA   2280

AAGTTAATGk TATGCTTATG ATCATCACCG CCTTGATCTA AAGCaTTAAA GTTTTAACTT   2340

TaTAATTTCA TCyTTTTaAT TcATATGAAA TTAAATTACC AATACTGATA ATAAACATAA   2400

aTAACATTAA TAAATTAATT TTTTGcACAT tGTGTTCCTT AATAAATAGA ATATTAACAA   2460

TATTATATCT TTATTAAGAT TTGCCCTAAA ATATAAAATT TTATTAAAAT ATAGCAGTAA   2520

TAAACGACTT TAAGAATATA AATGGGAATT TCTTGCAAGA AAAACCTTTT TGTAATTTAC   2580

ATTTTTAATT GAGAATATTT ATTATAGACT TTTTCCGCTA TTGGTTTTGT TTTTTTAATG   2640

TACTCTAAAT ATATGTTGAG GGTACTCTGA GCTCAGATTT TT   2682

(2) INFORMATION FOR SEQ ID NO: 48:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 2532 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CGGCATnACC AGTAAAGTTC AACACTAGAA TATTGCCTTA AATGCACGTA TAAATCCTAA   60

TTTTAAATTA GCACACTCTA TATCTAATTC ACTTATAACT TTCCtAGCGT TAACTTCTGA   120

TTTAAAAGTT TGTGATAAAA GGTGTTCTAA AGTATCTTCA CTAATTGTTA CTCTAGAGTC   180

TTGGTTAACA ACACTTTCTC CACTTTCCCA TTTTTTCCTC ATCCTCCACA CATTTACCCT   240

AGAAACCCCC AATTTATCCG CTATTTCCCT ATCATCTAAC AATCCTTCTC TAAAATATGC   300

AACATAATCA TCAAAGACC TTTTGGCTCT TTTCAAGAAA ATTCTCCTAA AATAACAAAA   360

TTAACAAATT GTTACTCTAA ATAGTAAAGC AATTTGTTAA TTCAATTAAC ATAAATTATT   420

AATTTCTTTA TACCTATTAA CAACTGCCCT ATATTTACAA TATTTATTAA TATAAAAACC   480

AAACATTTCA AATATCCAAA AAGGAGCATT TATATGAATC AAAAACAAAT ATTTTTATTA   540

TTTTTATTAT TTTTAAAAGT AACAATAAGT TTTTCTTATG ATCAATCTCA ATACAAGGGA   600

TATATGGAAA AATATTATCA TAAGAAAGGC AAAACAGATA CGCACATATC CTTTTTTCAA   660

ACTCTTAGTG CTGATGAAGG GGGTTTTTCT ACTATCTTTA TAGGAGAAGA TGAACAATTA   720

AGTCGTCTTA GTTTTACCAC TTTAAAGGAT ATTAAAGACG GCAAAGAAAC CTCTTATATG   780

GGTTTTAACT TAGAATACCA TTACAAAGCA AAGTTTAACA ATCCATACCC TATGTTAAAT   840

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GATATACGTG  CAAACATTAG  TAAAGTGAAA  GTTAAATTTT  TTTTTGATAA  TGGCCCCGAA      900

AAAATAATAA  GAGAATTAAA  TCAAAAATTT  GTAAATAATA  GAGTTATGTG  GGAAATTTGG      960

AATAATTCAT  ATAATAAGCT  TTCAGAATAT  ATTAGGATTA  ATCTAAGAAC  CTCTGATCCG     1020

GGCATAGAAA  ATTTACTGCC  AAAATTATTA  AAACATAAAA  CCGTAACAAT  AACAATTGAA     1080

ATTCCTGAAA  GTGAAGATCC  TGAGAAATTA  ACTAGTTCTA  TAACTTTTGA  TCTTGATAGC     1140

TTTCAAAAAC  TATACAAGAA  ATATAGTACG  TATTTTAAAT  AATATAACAA  GACTCGCTGT     1200

GAGTCTTGTT  ATATTATAAT  TTATGATTGT  AAAAAAAATT  TTTCTATTCT  TTTTTATTAG     1260

AATCTTTAGA  TTCTTTCTCT  AACTTTTTAA  GCTCTTCAAG  CTCTTCTTCA  ATCTTTTTAA     1320

GCGAGCTTAC  TATTATTTCT  TTAGCTATAT  CGCTAGTACT  ATTACCACTA  GAAATATTTT     1380

TAAAGCCCAA  ACCCCGAGCA  TGCCGCAAGG  nTTCTATTCC  AACTTTCCCT  TGATTTTTAG     1440

CCCTTTCTCC  ATCAGTTATT  CCAATTGCAG  ATTCAACTTG  ACCCTTAAGT  TCTTCAAATT     1500

TTTTTTGAGA  CTCTTCTAAT  TCTTTTTTTC  TTTTCTCTAT  TTTTTCATTT  AAAGCTTTCT     1560

CAAGGATTTC  TAATTCTTTT  TCAAACTTTT  CTTTATCTTT  TAGTTTTTCC  TTTAATTCTT     1620

CTATTTCCTT  TTCATAATCA  GAATATGTTT  TAAGAGAAAC  ACTTTTAGGA  TCCGACTTCT     1680

CTATCTTATC  CTTTAATTCT  TTTATTTTTT  GTTCAATTTC  TTCTTTTAAT  TTTTGATCTT     1740

CAGCAACACC  TTGAACCACT  TGATCTTCGC  CCTGCTCCTG  AGGCTCATCA  GCTTGCATAG     1800

ATTCTTCATC  CTTTGGTTGA  ACTTTTGCTT  CTGGTTTTTT  AAAATCTCCA  AAAAACTCTT     1860

CTTTTTTTGT  ATCTAAAAAT  CCCTTAACTT  TTCCTTTTAA  ATCTTGTTCT  AAACTTTTTT     1920

TTACATCTTC  ACCACTTGCG  TAATTCTTGC  AAGAAACTAT  CAGCGCAAAA  ATAGCACAAA     1980

TAATAAACAT  TTTCTTATTC  ATAAGTTGCT  CCATAAGTCT  TAAATCTAAC  GCAACACCGA     2040

ATAATTACAA  TTTTTCAAAG  ATTTAAATAT  ATAATTTTGT  TACATTCAGC  TATTACATAT     2100

TAACAAAACG  CAAATATAAT  TTTAACCAAC  TCCCCAAAAT  CTCTCCATTG  CAAATGCACC     2160

ACTCATTACA  AAAGACTACA  AAATCCATAC  AACTTAAATT  TCAAAGTCTT  TGCTATATAT     2220

TAGATAAAGT  ATACTGTCTT  TCTTATCCGA  CACCCTCAAA  AAATGCCTAT  TCTGTTTATC     2280

ACAGCCACTC  CACAACCCAA  ATTTCGCATG  CAATGAGAAC  ACCCAAAATT  TGACTAAAAT     2340

TTTAGGTTTT  TGATAAAATA  TAAATTACAT  TTTTATTAAA  TTTTTATTAC  TTTTACTTAA     2400

TTTAAAAGTA  ACACTTCTAA  GGAGAGGATT  TTATAGATAT  GAATAATTAT  TTTAATTTAA     2460

ATAATTTCAA  TATGGATTTT  ATGCTCAAAC  TATTTCAAGA  TTATCAAAAT  GTGGTAAATG     2520

AAAATAAAAT  TC                                                            2532
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(2) INFORMATION FOR SEQ ID NO: 49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2528 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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nAGGATCCCC AGCTCCCttA ATAGCCCCCa TCAGCCTTCC CTTTCTCACC ACCATCCTTC       60

ACAGCAAACT TTCCATCCTT AGCCATCCCC CTCAAAGCAA TAGCAGCAGC AATCTGATCA      120

TCCTTCTTCA TCTCATCCTT AAACTCCGCA CCATTCTCCT CATTACCCTT CCCAATAGCA      180

GCAGCAATCG GATTTGTAGC ATCCCCAGGC TTCTTTCCCT CCTGATCAGC CGCATCAGCA      240

GCCTTAACAA TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC      300

TTGCTAGCAG CCTCACTGTC CCCAGCATTA GCACCAGCAC CAGCCTTCCC AAACAACTTC      360

CCTGCCCCTT TATTACTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTC ACTCCCCCCA      420

GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCG TCACACTCGC CTTATCAGCA      480

ACCTTTGCAG CACCAGCATT AGCCACAACT TCTCCAATTG CATCAGTACC ACTTGAAGCC      540

CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA ACTCAGCAGC TCCCTTAATA      600

GCCCCCTCAG CCTTCCCTTT CTCACCACCA cTCttCACAG CAAACTTTCC ATCCTTAGCC      660

ATCCCCCTCA AAGCAATAGC AGCAGCAATC TGATCATCCT TCTTCATCCn TCATsmTTAA      720

ACTCCGCACC ATTCTCCkCA TyACCCTTCC CAATAGCAGC AGCAATCGGA TTTkTAGCAT      780

CCCCAGGCTT CTTTCCCTCC TGATCAGCCG CAtCAGCAGC CTTAACAATC GCACTTAATA      840

TCTGCTCCCC ACTAACAGCA CTAACAGCAC CAGCCGCCTT GCTAGCAGCC TCACTGTCCC      900

CAGCATTAGC ACCAGCACCA GCCTTCCCAA ACAACTTCCC TGCCCCTTTA TTACTCTCCC      960

CTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCCAGC AGCTTCAACA ATCTCCTTTA     1020

TCCCCTTAGC AATCCCCGTC ACACTCGCCT TATCAGCAAC CTTTGCAGCA CCAGCATTAG     1080

CCACAACTTC TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACAGCTT     1140

TTACCAGCTT ATCCAACAAC TCAGCAGCTC CCTTAATAGC CCCCTCAGCC TTCCCTTTCT     1200

CACCACCACC ACTCTTCACA GCAAACTTTC ATCCTTAGC CATCCCCCTC AAAGCAATAG     1260

CAGCAGCAAT CTGATCATCC TTCTTCATCC CATCATGATT AAACTCCGCA CCATTCTCCG     1320

CATCACCCTT CCCAATAGCA GCAGCAATCG GATTTTTAGC ATCCCCAGGC TTCTTTCCCT     1380

CCTGATCACC AGCAGCCGCA CCAGCAGCCT TAACAATCGC ACTTAATATC TGCTCCCCAC     1440
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TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC ACTGTCCCCA GCATGAGCAG        1500

CATCAACTTT CCCAAACAAC TTCCCTGCCT TTTCATTGCC CTCTTTAGCA GCAGCAACTT        1560

TCAGCTTTTT ACTCCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT        1620

TCACACTCGC CTTATCAGCA ACCTTCGCAG CATTATCATC AGCCACAACT TCTCCAATTG        1680

CAGCAGTACC ACTTGAAGCC CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA        1740

ACTCGCCAGC TCCCTTAATA GCCCCCTCAG CCTTCCCTTT CTCATCATTC TTCACAGCAA        1800

ACTTTCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC AGCAATCTGA TCATCCTTCT        1860

TCATCTCATC CTTAAACTCC GCACCATCCT CATTACCCTT CCCAATAGCA GCAGCAATCG        1920

GATTTTTAGC CTCCCCAGGC TTCTCTCCAT CCTGCGCAGC CTCACCAGCA GCCTTAACAA        1980

TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC TTGCTAGCAG        2040

CCTCACTGTC CCCAGCATTA CCAGCACCAG CCTTCCCAAA CAACTTCCCT GCCTTTTCAT        2100

TATTCTCCCC TTCAGCAGCA GCAACTTTCA GCTTTTCACT CCCCCCAGCA GCTTCAACAA    ·   2160

TCTCCTTTAT TCCCTTAGCA ATCCCCGTCA CACTCGCCTT ATCAGCAACT TGGCTTTTAC        2220

AATTAATAAA AACAAAGAAA GTTGTTAATA AAATTGCACT TGAAATTTTT TTCATATTTT        2280

TTTGTTTAAT GATTGTTTTG AACATTTAAA AAATGTTTTT GTTAAGAGGC TTTTATTCTT        2340

TGTTTAAGTT AAAGTTAAAT AATAATAACT AGTTTTTTTA ATTGGATTTG TGAATTTTGC        2400

CTACTTCCGT ATCACATATA ATAAAGTTTG ATGACATATA TAGTATTTTT ATTGCTTGAG        2460

AGTTTTAACA AGTGTAGGTG AGAGAATTTT TCATTTCTTT TATTATAAAG AATAAAAGAA        2520

ATGAAAAA                                                                2528
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    (2) INFORMATION FOR SEQ ID NO: 50:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 2496 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

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TGCAGGTCGA CTCTAGAGGA TCCCTGCCTC TTyaAGTATG CTAGCCAAAA TATRaCGAGT            60

AAwTTCTTTG TCTGATACTT TAAATTCTTT GTCATATATA TTTTTTkcAA TTTTAAATAC           120

TATAGArTCA TCAGGcTcTC ATAAAGyATC TCTCTAAGAG TTTTTTGAAT TATmTCTTTT          180

TCtTTrgAtA TTTGyTCTTT TTCAACTGmT ATTAyATTrC TTGTyTTTAG GTATCTTTCT           240
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1027

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TTTCTTATAA GATAGCTAAA TAAAATAAAC CATTCTTGCT CTTTATATTC TTCTTTtTCT      300

TTAATTTTAG AAAAATCAAA TTCAATATAT CTTTTTTCTC CATAAAGTAC TTTCGATTTA      360

TCATATAATC TCCATACCTT TCCATTTGAA AGTATCCCAT AATGTTTTTG ATATTGATTT      420

AGATATCTGT ATAGCTGATC TTCTGCTTCT TTTACCTTAT CTTTAGCATC AAAACTAAAT      480

GATGGACGCT TAACTTCTGC TATAAGCAAG ATATCTTCAG TTGGAATAGA TTCATTATTT      540

TTTTTAGCTT CTTCTAATTT TTTATTAAAA GCTACTTTAT CTTTATCATT TTCAAAAAGT      600

AGTATATCTA CTCTGGATTT TACTCCTTCT ATTTGCCCAC CTTTTTGTTG TTCTACTGAA      660

TAAGCTAATT CTTCAAATAT AGACTTTAGC AAAGACTCTA TATTTGCTTC TGTTGAATTG      720

TCATCTATAG CTTGAATTTT ATTTTTTAAA AAAATAAAAA AGTTTTTTGA TTTAACAATA      780

TTTTCTTTTT TTATAAAGCC TTTTGACAGT TCTTTATAAA GAGATACATT TGGATCATTT      840

GTTTTTATAA TGAATCGGCT TTCATTGTTC ATATTTACAA CCATTATGTT ATTTATAAAT      900

CCTTTTTAGC CCTTCTTGAT ACTCGAAATG TACTCTAAGA TTAGTTTTTT TAAAATTAAA      960

AAAACTAATC TTAGAGTAAG TCGGCCAAAA CTTGTTTTAA TATTTATTTG ACTATCAATA     1020

CTCTATCTTT AGAATAAGCT TGTTAAAAAT TATTTCTCAC TTTTTCTCAA TTAATTAAAG     1080

TTATTAATTT ATTTTTTATA AGGCATCCTT AATTAAAGAG CATTTAAAAA ACACTTTTTT     1140

AAAACCGAAT TTTTCTTAAA CATTCCCCAA TTTGTGAAGC ATAAACAAAA AAATGTTTTT     1200

ATCCTTTTCA TTTTCAAAAT TACAATTATA GAGTCTTTTG TTAATTTCTT CTTTAAAAAC     1260

ATCTTGCTCA GAATCATGCA AGCAACAAAG ATGCAAAAAA TTTTTAAAAG AACTTATCAG     1320

GTCAAAAACA ACACAAATAA TAACCCAGTT TTTATTCATA ATTATCCTCT CTCAAAATTA     1380

AAAAATAAAT CAAAGTCTTT GATTTACAAT TTTTTATTAA GCAGTGAAGG GGGAAAAACA     1440

AATTGTCCTA AATATTTAAC AAAAAATGGA AATAGACTTA ATAAACTTGG TTTTTTCTCA     1500

GGAAGGATTT CTAATTACAA CATCAAATTC TTCCTGAATA TCTGGAAACT CAATTCCATA     1560

GTAAAAAAAT TTATAGTAGC CGCTTAATTT TCTAATTATA TCTATTTTTT CTTTATCTTT     1620

ACTAGAAGTT TTATTGCCTA AAATATTTTC AATTAAACTA ATTAAAGCTG TAATATCACT     1680

AAATTTTATA TTTAAAGATT TGTCAAAGA TAATGAATAA AGTTTAATTA AAGAAAATAT     1740

TATTCCTAAA TTATCTGTAT CTTCACTTTT CTCATATTCT TTATATATAT TTTTAGATCT     1800

TTCTATATCT TCTTTAGCAG TATCGTTAAT ACCTCTAATT TTTTGATAGC TATATTCTAA     1860

AATAATTGTA ATTTCTTTAA TTCTCTTTTT AAATAAAGAA AATCCACCTT CAAATTTCTT     1920

TTTTTTAATA TCAAAAAATT AATCTTTGGC ATATCCTAGT AAAGGATTTC CTACTTTTAT     1980

ATGATGTTCA ACAAAGCTTA ATGGTGTTCC AAAAATAAAA TATTTTAATA ATCTAACTTA     2040
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TTTTTTTGAG ATAGTTTTTT ATAAAACTTG CCCAAGCAAT CTATACTCTT AAGTTCGGGT   2100

TTTCTCAATC ACCTATAACT TTATTTGCTA ATTAATTTTT TATAAAAGCT ATCCTTAAAT   2160

TTTTCAAAAT ATACTATATG AACTACTGCT TAAAAAGCAA AGACTATAAA ATAAGTAGTT   2220

CATCAGAAAG TTTTTGATGG TATTACTACT ATTAATAGAA TTTAAAAAAT CGAGCTTACC   2280

AATGTATTTA AATAAACTAG AAAGCAAACC ACAATACATG ATTAAAATGA TATGGGCAAT   2340

AAACTTAAAA AGTTTAACGA TAATTTTGAA ATTCTTATTA GAATCTAATT AAAAATGTAA   2400

ATTTATATAA ATTTTATAAA TAAAGAGTCA AAGAAACGC TTTATACTAG AAAGTCTTTA   2460

TAAAGATAAT AAAATATATT TTTTAGAACT TTCTTC   2496

(2) INFORMATION FOR SEQ ID NO: 51:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2487 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ATTTATTTAC ACGAAACCCT GACTTTTTGA GAAGATTTTT GAATTTATTA GAAATATGGA   60

TAATGCTAAT TTGGTTGTCT TTAAACTTAT GTTTGGATTT TTGAAAAAAA TAAGTACGTC   120

TTGTATCAAG ATTTTTCTCA TTAAAATGAT TTTTGTGTGC TGTTTGGATA GCCTCGAACT   180

CTTCTGAGTT GATAACAATT TCTCTAATAC AAGTTACATT TCTTTTTTTT GCCACATTTA   240

CTTTTATGTT GTATAAAGTT TTTCCATTTT TGCTTAAAAA AGTTGAAATA TCTTGCATTT   300

TTACTTTTTG CAGTTCGGTG CCCCTGCAGC CACTTATTGC GAGTAAATGT AAAAACCAAC   360

CAGATATTGG ATCAGCTTGT TTAAGAGTTT TGATGCATTT TTCAATTAGT TTGCCAATTT   420

TTGGGGTCAA ATAAAATTTA GGAGTTGGCT TTGAAGCTTT TTTAGTAGGC TTAGAAGAAA   480

TTTTTAGTGA ATTTTTAAGA ATTTTGTTTT CATTTATTAG TTTTTGATGA TCTTGTAATA   540

ATTTAAGCAT AAAATCTATG TTGAAATTAT TTAAATTAAG ATAATTATTC ATGTCCATAA   600

AATCCCCTCC TTATAAGTGT TACTTTTAAA TTAAGTAAAA GTAATAAAAA TTGATTAAAA   660

ATGTAATTTA TATTTTACCA AAAACAAAAA AATTTAGTCA AATTGTGTGG CTTCTCATTG   720

CATGCAAAAT TTGGATTGTA GGATAGCTGT GATAAACAGA AGAGGCAATT TTTAAGGGGT   780

GCACTTAAGA AAGATACTAT ACTTTAAGTG ATATATAGCA AAGACTTTGA AATTTAAGTT   840

GTATGTGTTT TGTAGTCTTT TATAATGAGC AGGCCATTTG CAATGGAGAG ATTTTAGGGA   900

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GTTGATTAAA ATTATATTTG CGTTTTGTTA ATATGTAATA GCTGAATGTA ACAAAATTAT        960

ATATTTAAAT CTTTGAAAAA TTGTAATTGT TTGGGGTTGT GGTAAACTTA AGGCTTATGG       1020

AGTGGATTAT GAATAAAAAA ATGAAAATAT TTATTATTTG TGCTGTATTT GTGCTGATAA       1080

GTTCTTGCAA GATTGATGCA ACTGGTAAAG ATGCAACTGG TAAAGATGCA ACTGGTAAAG       1140

ATGCAACTGG TAAAGATGCA ACTGGTAAAA ATGCAGAACA AAATATAAAA GGGAAAGTTC       1200

AAGGATTTTT AGAAAGATT TTAGATCCAG TAAAGGATAA AATTGCTTCA AATGGTCCAA        1260

TAGCAGATGA ATTGGCAAAA AAATTACAAG AAGAAGAAA GGTAAATAAC GGGGAAGAAG        1320

AAAATGATAA AGCTGTCTTT TTAGGAGAAG AATCAAAAGA GGATGAAGAA GAAAATGAGC       1380

AAGCTGTTAA TTTAGAAGAA AAAAATGCGG AAGAGGATAA GAAAGTTGTT AATTTAGAAG       1440

AGAAAGAATT AGAAGTTAAA AAAGAGACTG AAGAAGATGA AGATAAAGAA GAAATAGAGA       1500

AACAAAAACA AGAAGTGGAA AAAGCACAAG AAAGAAAACA ACGACAAGAA GAAAAGAAAC       1560

GAAAAAAACA AGAACAGCAA GAAGAAAGA AACGAAAACG ACAAGAACAA AGAAAAGAAA        1620

GGAGAGCTAA AAACAAAATT AAAAAACTTG CGGATAAAAT AGATGAGATA AGTTGGAATA       1680

TTGATGGTAT AGAAAGTCAA ACAAGTGTAA AACCGAAAGC AGTTATAGAT AAAATTACGG       1740

GGCCTGTATA TGATTATTTT ACCGATGACA ACAAAAAGC TATATATAAA ACATGGGGAG        1800

ATTTAGAAGA TGAAGAAGGC GAAGGATTGG GAAAATTATT GAAAGAATTG AGTGATACTA       1860

GAGATGAGTT AAGAACCAAA TTAAATAAAG ATAATAAAAA ATATTATGCC CATGAAAATG       1920

AGCCTCCTCT AAAAGAAAT GTAGATGTCA GCGAAATTAA AGAAGATTTA GAAAAAGTAA        1980

AATCAGGATT AGAAAAGGTT AAAGAATATC TTAAAGACAA TTCTAAATTT GAAGAAATTA       2040

AAGGATACAT CAGTTACAGT CAGTAATTAT ATTGGATGCT TTTAGATGTA ACTAAATTTT       2100

ACGTACACAA AATAACAGCT AGTAGAAAAG TTCACTGGCT GTTATTTTTT TGTAGATTTC       2160

ATTGTTATGA ATATAGAAAT GTTTTCTATC AAAACTTTCA TTTAAAAAGT GCAAAAACTA       2220

TTGCTAAAAA TGTTGTTTAT TTATATACTC TCTAGAGCTA TGACGTATAC AAATGAGATT       2280

TCAGATTTTG ATGATAATTT ATATAAGAAA ACAAAAAAAG AAATAGATAA ACTTATAAAC       2340

AAGCTCTATT TAACTAGCCn AATAACTCTA AAGCAAAAAA GACAAATnTA CAGTGCTGTT       2400

GAAAGAATGC AAAAATACGT AATAAAAACC GGAAAAGTG TTCTTTTAGA ATCGGAAAAA        2460

GAATTTGTTA AAGACACTTT GAAAAGA                                          2487
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(2) INFORMATION FOR SEQ ID NO: 52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2462 base pairs
        (B) TYPE: nucleic acid

1030

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGGAGATAAG TTTATTGGTA TTTTTTATGG CTATAGAAAC CCAATCAAAA cCTTTAATAA   60

AGTATaAAAT AAATGGAACT AGAAAaGCAT ATGCATTAGC AAGAGCaTAT TATATGGAAT   120

TTAGATTTAA AGCCgGAAGT GTTTTTTGCT ATTTTAAGGG CTATATCGT TTATTGGATA   180

AAAAAAGAAC AAtAATCaTT ACAACAAAGT TTTATTTAGT ATGTTTGCaG ATTTAGaACA   240

ACAAGTATAT AAATTTTATG GGAAAAmATA CCCGGAGCaA GGACCGTTAA TAAAATGGAT   300

AATAAAAAAC CTAAAATAAT AACAATAGCG TCAATCAAGG GCGGTGTTGG TAAAAGCACA   360

AGTGCCTTAT TTTATGGCAA TATTTTAGCT AAAGAAAGAC ATAAAGTATT GATAATTGAT   420

AGTGATCCAC AGGCCAGTAT TACTAGTTAC TTTTTGTTTA AATTAAAAGA ACAAAATGTG   480

AATGTCGAAA ATTACAATCT TTATGAAGTT TTTAAACAAA GAAAATATAT AGAAAATTGC   540

ATTTTTACAG TATCTAATTG TTTAGATATA ATTCCCAGTT CCTTAGAATT ATCTGTTTTT   600

AATTCAGAAA GCATACCATT ACAAGACAAC CTTTTAGAAA AAGACTTTT GACTATTAAA   660

TCTAAATATG ATTATGTGAT AATCGATACA AATCCCAGCT TAGGACATCT TTtAAACAAT   720

GCTTTAGTAA TTACCAATTA TTTAATAATA CCAATTAATT CCGATTTATG GGCAGTTGAA   780

AGTATAGATC TAATATTAGA TGCAATAAAT AAAGTTTATA GAAATGATAT TACACCTTAT   840

TTTTTAGTGA CGGGGGCACT AGAGAGACAA AACATAGATA AGGAAATAAT ATTTAATTTG   900

GAGAATAGAT ATAAAGAAAA TCTAATAGGA GTTATTCCTA AAGAGATGA TATCAAAAAA   960

GTGCTGTTTT ATAGAAAAGA ATTTTCTTCA AAAACAGACT ATTATCAAGA ATATAAAAAA   1020

TCTTTAGATA AAATGTTAAA AATAAAATAA CAAATAAAAT ATATCCAGTA ATGGACAAAT   1080

AAGGAGTTTG CATGAGCATT AAAAATAAAA TGATAATAAC CAAAAGAATA GATATAAAGG   1140

AAAATATGTC TAAAATGGAG TCATTAGAAG AAATTCATAA AGAAGAATAT TTGAGATTAA   1200

AAGACAAATT AAAAACTCTA ACAACGGATG ATATTTATAA TAAAATAGAA ACAGCAAAAA   1260

TATTAAATGC GATTAATCAA AAAAAACTGT ATATTTTAGA CGGATATAAA AATTTTTATA   1320

GCTTTTTAGC TGATTTTAAA ATCGCTAAAT CTCAAGCATA TAAATATATA AAAATAGTAT   1380

CGGGCGTAGA AAAAGGTATT ATTGACTATA ATTTTATTGC TAATAATGGC ATTGAAAAAA   1440

CAATTAAACA ATTGGAAAGT AACAATGTTA TTAAAAAATC TAGGCAAAAT CCAATAAAGC   1500

CTTTAAGGTT TCAACTTAAA AAGCAAGAAA GTTATGATTT TTATAAAAAA AATGGGAAGT   1560

1031
TTACTGGGTT TTTATTGGAA GAACTTCTTG AAAGTCAAAC AGATTTGATT AATAAGCTTT 1620

TAAAAAAATA TAAACAATTA AAAGGATATT AAGAGGATTT TATGAGAAAT TTGGTGCACA 1680

GAACATATGA TATAGAAAGC ATAAAAAATG AATTTTTAAA CATAGGATTT AGTGAAGAGG 1740

CAATAGATTT TGTTTTTCTT CATAATGATA ATTACAACTA TGAGGTTTTA AAAGAGAAAA 1800

TAATTGATGT AGAAAGAAT TTGCAAAAAG ACATATCTAG TTTAGATACT AAGATAGATA 1860

ATGTAGAAAA GAATTTAAAT GTTAAGATAG ATAATGTAGA GAAGAATTTA AATATTAAAA 1920

TAGATAGTGT TAAAAATGAA CTTAATTCTA AAATAGATAG TTTAGATACT AAGATAGATA 1980

ATGTAGAAAA AACTTTGCAA AAAGATATAT CTAGCTTGAA TACTAAAATA GATAGTGTAG 2040

AAAAAACCTT ACAAAGGAT ATATTTAGCC TAGATAATAA AATAAATGTT TTAAAAAACG 2100

AACTTACTGC AAGTAATAGA ACAATACAAG TAATTTTAAT AATGGGAATA ACGCTkGCTC 2160

CAATTATTTA TTCTATATTC AATAAGCaTT TTTTAAATTA AGAaTGATTA rAaTTTTATA 2220

AaGTAATAAG TTAGTATATA GCTTtAAAGT AGAACTTATT TGAATTTTTT AACAAGAGAA 2280

TTTAAATAGG TTCTTTTATT TTAACAAATA CAAATAATT TTAATTCTAA ATTGAACTGA 2340

ATTTAATTGT TTAGTGAGTT TATCTAAAAT AAATTGAGCT AAGCCAGCGG CTTTCTTAAG 2400

CTCTTTAACA TGAGAATTTA ATAAAGCTTT TATTTATTAT AATAATTTCT GTAAAAAGCn 2460

TG 2462

(2) INFORMATION FOR SEQ ID NO: 53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2447 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

AACCCCnAAA AAGGGCTCCC AATATTAAtw GAGAGATTTA TATTTTTCrA ATGTTGTGCT 60

AGCTTTTATy TCATTATTAT TGAATATAGG AGTAACTAAT GAGAAATAAA AACATATTTA 120

AATTATTTTT TGCAkCAATG TTATTTGTAA TGGCTTGTAA AGCATATGTA GAAGAAAAGA 180

AAGAAATAGA TTCATTAATG GAGGATGTTT TAGCTCTTGT AAATGATTCT TCTGGAGGCA 240

AATTTAAAGA TTATAAAGAC AAAATAAATG AATTAAAAGA AAATTTAAAA GATATAGGCA 300

ATGCrGAGCT TAAAGAAAAA CTATTAAATT TGCAAAATTC CTTTCAGGAT AAATTAGCGG 360

CCAAATTAGC AGCGTTAAAA GCAGCTAAAA ATACCATTGA AAACATTACT GACAAGGATC 420

AGGATATTTC AAAAAGAAAA ATATGGTCAG AAGCAAAATT AGTTGGAGTA ACTGTACCAC 480

TTCTTGGAAG CAATACTTCT GGTAATGGGG ATAAAATGTC TAAAAACGCT GTAGAACAGA   540

TAGACAAAGT AATAAAGTTC CTCGAAGAnG GCACTAATTA ATTAGCAAAT ATTCCTGTTG   600

AAAATGTTAA AATCTAGATA TTAAATCTGC GTCAATCTAA TATCTAGATT TTTCTTTTGT   660

TGCAAAAGCC GATTTGATCA TAAATTAGAA TTTCTTGCAA GAAAAACCTT TTTGTAATTT   720

ACATTTTTAA CTTCGAATAT TGATGATATA CTTTTTCCGC TATTGGTTTT GCTTTTTTAA   780

TGTACTCTAA ATATATCTTG ATGTTATGTT TTACCGCAGt ATAGAGTGTT CGTCTTTTAG   840

TGTTGATAAG TCTGGATAAG GATATTCTGG ATAATTGGGG TCATTAACTT TCACTTTTGT   900

TTTAGCTAAA AATGTTACAA GATACATAAC ATATTCTGAA AGTTGTGTTT CATATTTAGC   960

TAAAGATTTT AGCGTTGGAA TAATTGGCGG TTTTGGTTCT TCTGGTAGGT TAGCAATAGT   1020

GGTGCAACAT AACAACAAAA CAATTAGTAA ACAATGCAAT CTTTTAAGCA TTTTCACTCC   1080

TTTTAAGCAT TTTGATGTAT TCTTTCATAA TTTTGTTGCG TTTTGCTTTA AGTGAAGTGA   1140

TAATTTTTTT ATTTTTGTCA TAAGAGATAG CCTCTATTAT CTCAATATTG TATTTTAAAA   1200

TGTCTTTTAT TTCTTCAAAT ATTTTAGTTG AyTCAGCTGT TTCCATAGAT TTTAGTGTGC   1260

TTATATATGT TTTATAGAAA AAATCTATTA CTTTACTAAA AGTATTAATG TAATTATGAT   1320

CTATGTTTGT ATCAGTTTTA GCTATGTTAG TTAAGCTAGA TAGTAAATTA AGTCCCAATT   1380

CAATAGTGTT CTTTTGCATT ATTTGCTCTC TCTTTGTAGA TAGGTTTTCC GTCTTTATTG   1440

AATTTTAGAT CATTGGATAT TTTTAGATTT TTATCATTAG AATTAACCAA ATCAATAACC   1500

GTATTGATTT TTGCATTTAA AGGAGCGAGT GCCGCATTTA TTGCTGGGGT TAATGCACTC   1560

TCAAGTCTTT CCATATTTGC TGTATAGATT AATTTATAAT GAGAATACAG CTCATAAACC   1620

AAAAAGAATC CTTTATGTGC AATTTCATCA AATTCATCTT CAAATTTAGA AAATATATCA   1680

ATAAGGGTTG ATAAAGACGT AAGTCCAAGC TCAACATTAT CTTTGGATAA TTTCATAAGT   1740

TAATCTCTTT TTTTAATGTG ATTTTTGCCA TTACCATTAC CATTCTTAAA AATCTTGCCT   1800

ATTACAATAG TCAATATGTC TTTTAGTAAA GGCTTGAGAA GAATTAATAC TCCTAAAACC   1860

AACACTGTTA CAAAAATCAT TACGGCTATA AGTTTAATTT CGTTTAAATT GATAAGAAGT   1920

TCTGTTAATT TAATAGTATC CATTTTTTAA TCCTTTATTT TAATTTTTTA TTTGTATATA   1980

CATTATATAT CAAAATCGTA ATTTTTGCTA AAAAAGCTTA CAGTTTTAAA AGATCTGGGA   2040

CTGAATCTCC ATACATGTAG GCTCTTTTTT GGATATACCA TCCGTTATAA ATGGGAGTTC   2100

TGGTGAATAG TCCGCGAGGG CCCGTAATTT CATAAACCCA ATTGTATGTA ATTTCATCAG   2160

AATACATAAG TTTTAATGAT TTTTTCTGCA TCCTATTATC ATTGATTTTT ACTTGAATCT   2220

1033

CAATATCAAG ATAAATGGGA TCATTATCGT AATTTTTGTA AAAAATAAGA GTTACATCAT   2280

CATTGTCTTC CATATTAATA GATATCGCTT TATTCTCATA GTCAGAAGGA TAAAGTGTAG   2340

TACTTCTAGT TATGCTGCCA TAAGTAAAAT TTGATGGTAC TCCAAGTATA TGTTTAGGAA   2400

CnGGTGTTTT TTGAATAGTA TCTGATGAAG GCATTATCAA AAGATCA   2447

    (2) INFORMATION FOR SEQ ID NO: 54:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2401 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TATTATTATA TTTAGGGAGA GAATTTATAA AATAAAGCAT AATTACTAGA ATACTTGTTT   60

TTTCTATGAA TGATTGTAAT GCGGATCTTA ATATTAATAA TTATAAAACC AAAACTAAAG   120

ATGGGTTTTA TGCTTTAATT TAATTAATTT TAAGGAAAAA CTAATTACCA TATTAATCCC   180

AAATATATAA TTATTGACAA AAGTTGTATC AAGGGATATT GCCTAATATA GCAGAAGTAT   240

ATTCTGTTAT TAAATATCTC CTAAGGAGGA TTTTATTTTT AAAATAATAG AAAATAGTGC   300

ACTTATTTTA ATAGATATAC AAAATGATTT TTTAGAATCA GGCACTTTGC CAGTATCTAA   360

CAGTAATGAA ATAATTTCTT TGATTAACCA ACTTCAAAAT TATTTCAAAA ACATTATTGC   420

CACCAAGGAT TGGCATTGTA AAAATCATGT AAGCTTTTCT AACAATAAAA ATGGGGGTAT   480

TTGGCCTGAG CACTGCGTCA AAAATACTTG GGGATCAGAA TTTCCTAATG ATCTAAATAC   540

GAAAAGAATA AAAAAAGTTT TTTTTAAAGG AACCGATCAA TATTACGATA GTTACAGTGG   600

ATTTTATGAT GATTGCATTA AAAAAAAACA AACGGGCCTT CAGCTTTATC TGAAAAACAA   660

TTCAATCAAT ACATTATTTA TAACGGGACT AGCATTGGAT TTTTGTGTAA AAGAAACAAT   720

ACTTGATGCA ATTAACTTGG GATTTCGAGT TTATCTAATA ACAGATGCTA CAAGAAGCAT   780

AACATCTACT CCTGAATTAA TAATTCAGGA ACTTAAAAAG CTTAATGTAT TAACTTGCTT   840

CTCCAAGGAC ATCTTCGACA GCCAAAGTAA GCTTAATATA TAAAAAATCA TTCAATAGTA   900

TTTAATTAGA AAACTACTAT TTATAATTAA AACTATCATG GAATGATAGT TTTTTAGACT   960

ATATAAGAAA AGTTTATTCA CCAAAGAATG GCCTTTATAT TAAATTAAAG CCGCCTTTTC   1020

CTTGGTTTTT ACTTCTTAGT AAGAATAATT TTAAGATTCA TAGTTACATT TATATCTCTA   1080

TCATATAAAG CTCTGCAATT AACACAAGTC AACTTAATAT TACTTATCCT TTGTGTAATA   1140

CCACTTCGAA TGCCCTATTT AAATATAATA AAAGAATGAT AAAGAACTCA AATACTTCCC   1200

CCATGCATCA TATAAAAATA TCCATCTCAA AATGTTAAAA ACAACGCCAC CGACATAATT   1260

CTCTAATACC CAATGTACAG TCTATAGATA CAATAAAATC TTTTAAGAAT TTAATTCCAA   1320

TAACACCTGT TTAAACCGGC TCACAATATA AAAAATTTTT ATTTTTTAGT GATAAACTTT   1380

ACTTATCTGA AAAATTGCTT TATTATGTAA GAGTGTATAA AAAACCATCC GAAGTTGAGG   1440

AGGCAGAAGT GAAGGTTAAT AAATCCCTAC AAATACAAG TAAATATCAA CACAAACTAA   1500

TTGCTTTAAT TGCGACACTT GAGTATATTA ATAAAAACAA AAAAAAATAC AACCAATCAG   1560

ACATCCTTTA TTGTTTTAAC AGTAACTTAA GGCGCAACGG GCAAAAGAA GTTTCAATCA   1620

AAACGCTTAG AAACTACTTC TATAAACTAG AAAAGCTAAA TATTACTATT AACTACTATA   1680

GACATCTAGG TATTAATATG GGCACTGAAA TCTACTATGC TCTTAGGCAT TCTAAAAAAG   1740

ACTGCTATAA TCTACTAAAC CAACACTTTA GGAATAAAAA AACAGAAAGA TTTCAAAGAC   1800

GTGTTAATGT ATATATTAAA ATAAATTACG ATAAAAAGGA CAATGTAAAA AATGGGGAGT   1860

GTCTTAATAA TAAATATAAA AAAGAAGAAA GAGAAACCGA AAGAAAAAAA AGGATTAATA   1920

AGCTTAAACT AAAAAAAATAT GCAAAAAAAT GTAATTTCGA TAATGAAATT TCCTCTTTTA   1980

TTATTAATCT TAACTTAAAA AAAGAAACAA CAATCAAGCT TTTTAAATTT ATAATCAAAG   2040

AAAAATATTA TTTCAAAAAA GAAACAAAT GTAATTTACA AAAAACACTG CAAAACAAAA   2100

AAAGAGATTT AATTTCAATA TTAAGAAAAA CCCAAAAAAT TTTAATAAAA GAAGGTTGCG   2160

ACAAAAAAAA GATAAAAACC CAAATACAAA ACACATATCA AAAATATAAA AACAAACCCC   2220

ATTTCATATT AGAAAGCAAT AAATATAAGG ATTTCGATCA AATTATAAAA AAGATAAAGG   2280

ACGATACTAA TAAAACCGAA CCCCAAAAAC ATAAAGACAA TATAGAAACC AATATATATA   2340

ACATACTTTT AGATCAATTA CATAGAAAAA CCAACACAAC AAATTTAAGG TCGGGGATCC   2400

G   2401

    (2) INFORMATION FOR SEQ ID NO: 55:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2324 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

    CAATATGACA TCCTGAGGAC CTTTTATGGA GACTTGTAAA GCTTTTTATT TCTAATGTTT   60

    TAGCTTTTAT AAAAACACCA ACCATGACAC ATATTGAATT TTTAAATCTA TAAACATTAT   120

1035

TTCCTTAAAT TTCTAAAAGT TTTTTAGGCT CTGTATTTAA AAAAATCACT TCACCAAGAA   180

TAACCTTTTC ATCATTTAAT AATAATGTTT TCTTGCTAAG AAAATTTATA AATCTATTTA   240

AAATGCTTAA TTAAGCTTAT TTGTTTTCAA ATAATTCTCA TATCCTTTTA TTAAAAACAA   300

AATGTATTCT TCTCCCTTTT TATTTTTTAG CACCTCAAAA TCATTAAGCA AAACCTCAAA   360

ATCTTCTTTG GTTAGCGAAT AAAGACTAGC TACAATAAAG TTATTTTCAT TTTCTTTTTC   420

TTTGAAAAAT TCATCTTTAG TGTCTAATTT TAGAATTTTA TTAACTTTTT CTTTGCTAAA   480

TTTAAAATGC TCTAAGTAAA GCAAATTAGA GAAATTTAAA GGATCATTTT TAGCTATTAA   540

CAAGGAAGTG TTTTTTACTA AAGTTAAGTA TATCGGATTA GCTAAAATTT CTTCTTCTTC   600

GGGTTGAGGC ATAGGGCATT GATATAAGCA TGATTTTACA ATATCAGTGC TTAAAGCAAA   660

TCTTCTTATT AAATAGTCAA AAACAAATGA ATTAAAAATA GATATAATAA ATAATTTTTT   720

ATAAATAGAT ATTGGTGTTT TCTCATAATT TATATATATT GTAGAAACAC AATAACAATT   780

TCTAGGAGAT AAAGTACTAA TCATGGTTCT TATATCTGTA TTTCTTGCAA TCCTTCTATA   840

TAATATTTTT TCTATTTGAT ACTGATTGTC TTTAGTTGAT ACTTTTTGAA AGTCATCTTT   900

ATCTATCCAT AGTAATTTAG AGCTTTCTTT TGCATCTTTG TCTTCAAAAA ATCTTGAATT   960

AAACTGATGA ATATTAGCTC CAGAATAAAG AAATATAAAA TTTTCATTAT TATATTCTTT   1020

ACATAGTGTT TTATACTTTG TTAAATTTAG CCCTACTCCA AAATTAATAT ATTCTTCACT   1080

AAGAGTACTA AATTTGCTAA ACATTTTGTT AATTAAGATA AGCTCTTTAC TATCTTTAAA   1140

TTCAATAATT GATTCTTGAA TAGGAGACAG TTTTTTAATT TGCTCTATAT CTAATTTAAT   1200

TCCTTTATAA GGATCATCTT TATTATTTTC TAAGTTACTG GTTATTTCTT TTAAAATATT   1260

ATCATTACTC TGAATCATAA ATTTTGCTTT AAAATTCGAT GTAGGAGTTT TAGTATTGCT   1320

TATTTGAAAT ATTGCAAATT TAAAAAGTGT TGCCACATCT TTAAATCTTT TTTGATTTTG   1380

AAATTGATAA ATATAGTTAA GCTTATAGTT AGTAAATATA TATTTTCTTA GTATCCTAGC   1440

ACTAGATTCA CTCCAAAGAG CTGAAGGAAC TAAATAGGTT AAATTTCCGT TTTCTTTTAT   1500

TAATTTCAAA TTAAATGCTA CAAAATATCT AAAAGATTT GGATCACCAC CACTAGCAAA   1560

ATTTTTAAAA TCGCTTTTAT AAAGATTGTT GATAGTACCC ATACTATTTT TTTCTTCATT   1620

GTATTCAATA TTCAAAGGAT GATTATCTCT GCCAAGTATT TCTTGCTTTA TTTTATTTTG   1680

TTCTTTTATG CTTAGCTTTC TATAACTGGG AATATGTTTT GAGAAAAACT CTGCTTCATT   1740

AAACTTAGTT TTTTCCCATG GAGGATTTCC AATTACAATA TCAAATCCTT CTTGAATATC   1800

TGGAAACTCA ATTCCATAAT GGAAAAATTT ATAGTGGCTA CTTAATTTTC TAATTTTCTC   1860

CATTTTTTCA TTATCTTCAC TAGAAATTTT ATTGCCTAAA ATATTCTCAA TTAAACTAAT   1920

TACAACTGCA ATATCACTAA ATTCTATATT TAAAGATTTG TCAAAAGATA ATGAATAAAG   1980

TTTAATTAAA GAAAATATTA TTCTTAAATT ATCTATATAT TTACTTTCTT CATATTCTTT   2040

GTATATCTTT TTAGATCTTT CTATATCTTC CTTAGTGGTA TCGTTAATAC CTTTAATTTT   2100

TTGATAACCA TCTTCTAAAA TAGTTGTAAT TTCCTTAATT CTTTTTTTAA ATAAAGAAAA   2160

TCCACTTTCA AATTTCTTTT TTGCAATATC AAAAAATTCA TCTTTAGTAT ATCCCAAGAG   2220

AGCATTTCCT GTTTTTATAT GATGCTCAAT AAAGCTTAGT GGCGTTCCAA AAATAAAGGT   2280

ATTAATCCAC AAACTTAGCA TAGTAATTTC AACCGAAATA GGAT   2324

(2) INFORMATION FOR SEQ ID NO: 56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2148 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TnAAATCTAG GATACCCCGA cAAATATTAT TTTCCAGTAA TTATGAATAT TTGCTCGTAC   60

GACAATGTAA AGAAATTGCC TTATGACGAG CTTTTAGAGG TCAATAGACT TGCTGAGATT   120

AAATTAGAAA AAGAATTGTA TGAATTAATT TTAAGCAAGT GAGGGCTTAG TGAGCGACAA   180

ATTCACCATT AAATTTAAAG GGATTCTTGA TCATGCTGCA ACAAAAAAGG CCATTGAACA   240

AGATATTTCT AAAATGGAAA AATATCTTAA ACCCAGAAAC TCCAGTTTGG GAAGCACTAA   300

AGATATTGTA AAAAATAATT TGTCGrACAA GAAAAAAGAA CTTAGyArAC AATCTAAATT   360

TGAAAGCTTA AGAGAGCGTG TTGAGAAATA TAGACTTACA CAAACTAAAA ArCTTATAAA   420

ACAGGGCATG GGrTTTGAGA AAGCTAGAAA AGAGGCTTTC AGAAGATCTT TAATGTCTGA   480

TAGAGACAAA AGGCrTCTTG AGTATAAAGA ACTTGCAAAA GAATCAAAAG CAAAAAGTAA   540

AATGTTAGCG GCCTCTCAAG GAAAAGGACT TGTTGCCAAA ATTGCAATAG GTAGTGCCCT   600

ArGGAATATC ATTAGCAACG CTATGAGTAA AGTTGGAGGA GGCCTTTTAG GTTTTGCTAA   660

AAAAGCrGTT GAAGAAGACA CCAAAACAAA AAGAACAAAA CTTCTCAATA GTGCATTTTT   720

TACAGATAAC GAACGAAATA TGATTATGGG AAATAAAGAC AAGAATACTA AGGGAATTCT   780

TGACGGAATG AArGGwTTTG AGCGmGACTT AGAAAAAGAA GArTTcTtAm ATCAAGCAAG   840

TGyCTTTAAG GGTACTyTAA GGGACyTAGA TATGTTAAAT GAAACTAATT TGAAAAACGC   900

aGTAGAATTT GCAGCTATGC TTAAATCCAG TGGTGCTATG AGCAGCGAAG ATGCAGTAAA   960

1037

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GGCTGTTAAT AGTGTTCTTG GGGGTGATGG AAGTGAGCTT TTtGATCTAT TAAAGAAGTC      1020

aGGTGTTGGA GACAAATATA TAGAAGATGC CAAAAkGGCy TGGCAArGCG GGGCwsArGT      1080

AGATCTAGAG TCyAGAATTA CCAAGATGAT GGAAATGTTC GAGGATTTTA AATCTTTCGG      1140

CCTTACAAAA AAAGTCAATA ATGCTGAGAG TATTCAAAGT AATTTGGCCT CAGCTGAGCA      1200

AACTCTTCAA AACTTAACCA CTACTGTCTT GGACCCATTA CTTGACCTCA TTAATAAGAT      1260

AACTAATTAC TTTAAAGACT TTGCGTTTGA AACACACATT ATTAATCCCA TAATTAATGG      1320

CATTAAAAGT ATTTTTAATC TTAATTATTT CTTTGCAAAA TTAAAATCGA TGCTACCTGG      1380

ATGGATGGGC GGAGATGAGG GTGCGGCTCT AAAAAAACTA CAAGAAGAAA TTCAAAATCA      1440

AGACAATGCT AACAGCACAC CATAATTTTT ACAAAGGTA ATTACTTATG ACAAGTAACA       1500

AAAAAATTGC TAACAATGCA GCTAACAAAA TAGATATTAA TAATAAAATT ACTAACAATC      1560

ATGATATTGA AAAGAAAAAA ATCAAGGAAA AAATyAATGA TATTGAAAAG AAAGAAATCA      1620

GGGAGATTAC TCGAATAATA AGAGATGTAA TAACCCAAAT ATTTGCCCTT TTCGGAGCAG      1680

ATAATTTTTT AGTGTTATTT CCTAGAATGG ATCTAAAAGG TTTTGGATAT ATTCCTCAAT      1740

TGTTTTTTAT AAAACCAAAA AATGAACTCA TAACACGCAC TTATAATACT AGTTGTTCTA      1800

AAAGACCAGT TATCAATTAT TATGATAGAA AAGCGGAATA TGTAAGCTAC AATCCGGTAA      1860

TGACTGGTGA ACATATCTCA TTAAACGGkG GAATACTAAC ATCCTTATAT AAGGATATGm      1920

TTTCTTTACT yAAAATGACT GTTTTTGGCA ATACTATGCT ACGTTTTGAC GCGCATCTTG      1980

TAAAAGAACA ACTAGCCAAT AGAATACAAG CACAAGTCCC TTTTAGTATm TATAGTCCAA      2040

CTTTTGGACT TAAAGAATTA GCTGTAATTA CAAGTCTTTC GTTTAAAGAT ACTCCTTTCA      2100

TTGACGAGTT GAAGGTTAGT CTGTCAATAG AAATAGTAAA AACATTCG                   2148
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(2) INFORMATION FOR SEQ ID NO: 57:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2123 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
ACATATTATT TTGTTTATTT TTACTAATGC TAAACGGCTG TAATTCTAAT GATAATGACA       60

CTTTAAAAAA CAATGCCCAA CAAACAAAAA GCCGGAGAAA ACGTGATTTA ACCCAAAAAG      120

AAGTAACACA AGAAAAACCT AAATCTAAAG AAGAACTACT TAGAGAAAAG CTAAATGATG      180

ATCAAAAAAC ACAACTTGAC TGGTTAAAAA CCGCTTTAAC TGATGCTGGA GAATTTGATA      240
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AATTTTTAGA AAACAATGAA GATAAAATAA AATCTGCACT TGATCATATA AAAAGTGAAC   300

TTGATAAATG CAATGGAAAA GAAAATGGGG ATGTTCAGAA AAATACATTT AAACAAGTAG   360

TTCAGGGAGC TCTTAAAGGG GGAATAGATG GCTTTGGTGC AAGCAATGCA ACTACTACAT   420

GCAACGGTTC CTAATAGCTA TTAGCCCCCT ATTTGGGGGC TTTAATCTTG CTATGCTGCA   480

AATATCTCAT CAAACCGTTC GTATTCTTTT AAGATACTAA AGAATATTAA TGGACTAGGG   540

CCATAAATAG GCCTCTTAAG CCCCATAAAC CTTTCAAAAT CTTGTAAATC CTTTAATCTA   600

TTATTTTTCT TGAAATAGTT TTTTATAATC TCGGCCCAAT AGTTTATGCT TTTAAAATCA   660

CTATTTTTCT CAAAATACGA GATTAAATCA GATTCAATTT TCTTGATATC ATCAAAATTA   720

TTGGGGTCTA TATTCTGAAT AAAGCTTATT TTTTGAATAA TTGAGTTTAT ATTATCTTTT   780

GTTGTAGGGC TATTTACCCA GTCTTTTATA TTAGACAAAG CTTCTTTAAA AACACCGTAA   840

TAATAAAGCC TATCTTTTTT TTGTTCTTGC TTAATATCTC TTTTCTGGTT TTGAATAGTG   900

TTATTTTTTT GAATTTGATT AATCTCTTGT TTTTGTTCTC TTTTTTGTTC TTGCTTTTGA   960

TTAACACTAA CTTGCTTGCT AGGCATAGAA TTTTCGTTTT CGTGGTTATT GTAAATAGGA   1020

GCTGCATCAG TATCTATTTC ACTTTCTATA CCAAGAGCTG CAACTAAAGC ATACCTTTTG   1080

ACATAAGTAA TGCCTGAACC AAACATCTGA TACACTGTAT TTGTAACTTT AGACCCATTT   1140

TCATTGTTCC ATTGTAAATT TTCTGTAGGA ATTCGCGTAT CAAAAGAAAA TTCATATCCA   1200

GTACTTGTAC TGTAGAATGT AGTCCTAATA TAATCAACTA TGCCATATTG ACCCTCTATA   1260

GAAATTGGAT ATTGCTCAAT ATCAAGCTCC AAATTGTGCT TTTTAATAAC ATTTTTAATT   1320

TCTCTAACTA TTTCATTGAA ATTTTGATAT TTATATCCAT ATCCTTTAAG ACTTTTGTCA   1380

ATCCCTGGTA AATTCATTTT TAGGGTTTTC ATATCTTTTC GGAAGCTTAT TTTTGCTTGA   1440

ATATTATTTT GTATTCTTG ATTATTGTTT GAAAGATTTT CCATCTTTTT ACTCCTATGG   1500

TTATTTATAA AAATAAGTAT ATAGCAAAAA CTATTTTTGC CAACTTTTTT ACAAAAAATT   1560

TTACAAAAAA ATAGGGCTTA GCTAAATTCT CTATTATCTA CTAAAGAAAT TAGTTAAGCC   1620

CGTGCTAAAA ATTTTTTTGC AAATTACCAT AGGTAGTCAA AACTGAAAAA TGTTTAAATA   1680

ACTACGCTGT TTGTAGTGTA GCCCAATTTT AAATTAAAAT CAATTTATAT TTTCACTGAA   1740

TTAAAAATTT CTATATTAAT TTAACAAAAT TAATAATTAA AATTTAATAT TTTTTTAGAA   1800

AAGTATTTAC TTTTAAATCA AAATTTTGCA TTATAATAAT TAATTATTAA TTACCATAGG   1860

AGAAAAAACA TGAAAGGTTT TTCAAATACC ACAAAAAATC CCACTTGCCA CAACAAACAC   1920

CAACACAAGT TAATATATCT AGCTTCAACA CTAGATTTtC TAAACAAAAA AGaTAAGAAA   1980

1039
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TACACACAAC AAAACATACT CTATTACTAT AATGrrAATC TAAAAAGAAA TGGkCTAGCT    2040

CCCACTACTC TAAGrACmAT GgCAAAATTA TCTTTACAAA TTAGAAAAAG TATTAAAAGT    2100

CACAACTAAT TACTAACCCn AAA                                           2123
```

(2) INFORMATION FOR SEQ ID NO: 58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2093 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
AAAAAAGTGC GCCGTGCGGC GGTGnAACGA CTCAATAGTT ACTAATAATC CATTTCTAAA      60

CTTAGAAATG CAAATTAATA ATATTTTCTA AAGTATTTTT TGTTTCCTCA TAATATGTTT     120

CTTTTACAGA AGGTTCTAAA AGTTCATTTA TAAGAACTTT TACACTATTG TAGTAATGAA     180

TTTTTCCCTT TATGTAAAAA GAATATTCCT TATAAAGCAG TTCTTCTACA TCTTTAAATG     240

TATTTCTATT TTTTAGAAAC TGATTTTCTA TAATCGAAAT ATTAAAGCTT TTATTTCTAA     300

AATCTTTAAT ATCATTAATG GTTTGCATTA AAATACTTAA ACTTTCTACA GAGAATCTTT     360

CTACTTGAAC TGGAATTATT ATATAATCTG TAACATTCAA AGAATTTTTT AAAATAAAAC     420

CCAAGTTGGG TGGGGTGTCA AGTAAGATAT AATCAAAATT ATAATTTGTA ATATTTCTAT     480

TCAAAATATT TTCTAAAAGA AGATCTTTAT AATTTAAAAT TTCTGAATTA AAATTTTCTA     540

AAATAGGATG AGATGGAATT ATAGAAATAA AATCATTAAT TTTATTAATA CACTGTCCAA     600

AATAAACATC TTTTTTTAAT AAGCTGTAAG AATTGCATTT ATCAATGTTG AAAATATATT     660

TACTAAAATA AGAACTTAAA GAATTCTGTG GATCTAAGTC AATCAATAGA ACTTTTTTGC     720

TTAAATCTTT TAATATATAA GAAAAAGTA TTGTTAATGT GGTTTTACCT ACACCTCCTT     780

TAGGGCTTGC AATTGTTATA ATGTTTGATT CTTTTCTATC CATTTGTTTA TTATTCCTTC     840

CTCTTTTATT TTTTTATTGT AAAATTCGTA AACTGTTTTT TCCATGTTTT TTATATTTTC     900

TAATGTAAAT TTATAGTATT TTGTTTGTTT TTTTTCTTTT CTTAGTAATG TCCATAGGGA     960

CTGAACGTAA CACTTAATAG ATCCTTTTTT AAATACATAT TCTATGTAAT ATGCCTTTTT    1020

TACTACATAT TTTATATTAT TATTGCCTAT GATAAAAAAA GGTTTCTCGA GATTATCCCA    1080

ACCGTATTTT ATGCCTAAAA ATTTTTCATC TTCTTTTATT GGAAATAGAT TGAAAAAATT    1140

CCATCCTCCA GTATCATTAA ATTTTTGGAA GGTTATCCTA AGACCCTTTC TAGTAATTTC    1200

AAATTTGATT AAATGCTTAA ATATTATTGA ATAATATGTT TTTTTATTCT CCTTTTCTTC    1260
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TATTTTATAA AAGAAGATTC TTTTTTTTGT TTTCTTTTTA AGATTTCTAA ATCTTTCTGT      1320

AAAGTTGTTC AAATTTTTTT CCTTTTATAA TTAGCTAGTA AATCAAATAG AAATGTTTTA      1380

TTTTGATTTA TTTTCCATTT ATTGATGTAA GTGTCTTTAA ATTCTCCTAC AATTTTGAAG      1440

AAATCTGTTT CGTAGTGAGC ATTTGTCTC ATGAAGTGAA TTTTATTTTT ATATTTTTTT      1500

AGCTTTTTTA AGTAAAACTC TTTTATATCT TTTGTTTGAT AGTCGTATTT TAAATGCTTG      1560

TTGAAATCTT TGTAATTTAT AAATAACAAT GGGGTTATTA TCAAGGCTGG TGGTGGGCCA      1620

CCAACCGCAA TTAATGCATA TGCCCTCTCT GATTCATTTA CAATCAATTT TGCACCCGAA      1680

GATGAACATC AAGATCAAGC TAAACATCCC AAACAAGAGT ATTCTATTAA TTTGATAAAA      1740

GTTGCAATTT TTGGCAATAG AGGCCTTGAG AAAACAGTAA CACCTGAAGC TGGTGGTTAA      1800

GCCTTGGGCA ATAAAAGGAG TTAAACAAAT GGCAGACACA ACGCAATTAT TAAAAGATTA      1860

TCAAGATAAA CGAgTAAACT TGAAAAGTTT ATGAAAAATC CCCAGTATGA CGCTGGTTTG      1920

CTTAGCAATT CtGTAGAGTT TAGAGATAAA AACATACAAT TTTTTGCCTC TGGAGGCACT      1980

AGAACCAGCA AATTtGACAA aTTAGAAAAT CATCCATTTT CtGGGTATCC ATACmAGCGg      2040

GGaTAAAAAG AGTTATTCAA GAGGAAAAAG CTGATCAAAT TCACTATGGA ACC            2093
```

(2) INFORMATION FOR SEQ ID NO: 59:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2019 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
GTCTTAGTCA TATTTTCATT AAGTCTTTTT GCTTATTCTT AGCAACCTCT AGCAAACTTT        60

TAGTACTACT CATTGAAGCT TTAGCATCAG CCATAAATTG GTGGTAGCCA GCATAGTAGT       120

AGCTCTCATG CCTTGAAGCA TTGCTATTAC TTAATGCCTC TTCTAAAGCC CGATCTGCTT       180

TTCTTTGTGC ATACTCAAAA TCGTTCTTAG CTCTTTTTAA AGCAGCAATA GCATCATTGC       240

AATGAGTATC AGCAGAAGCA TGATTACTCT TAACCTTAGC AATAGCTTCT TCTAGGCTAG       300

GCAATAAGGC TAAGTTAGCT TTACTAGATC CCACACCTCT TCTAGTCTGC TCTAAATAAG       360

ATTTAGCTGT ACTAAGTAAG CTTTTTATCT TATCAAGGCT TGCTTTTACT TTTGCTAAAT       420

CTTCATTTAT TCTATTGTAC TCTTCTTTAG AAGATTCAAT TTCCGTCATA ATGTTTCTAG       480

CTTCACTAGC TTCATTATCT TGGATATTAA CTTGTAGAGT ATGGTTGCTG CTACTATTAT       540
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CATTTTGCAT ATCGGGTTGC ATGTCTGCCA TCAAAGGTTT TTTGCCTGTA TCTTGGTCCA      600

TATAAGTATT ATCTACACTT CTAGGCTTAC GACCACTTCT CTTGCTGTCA TCGTTACTCT      660

TTAGAGTATT AAAAGACCCA TTATTGCTTT TTAGTTTGTC TATAACCTGA TCGGCGTTGT      720

ATGTAATCTT CTTGTATAAT TTACAAGAGA TAACACTGGA AAATAAAATA GTTAGAATAA      780

ATAATTTATT AATTAAATTC ACCTTATTAC TTCTCTTTAG AATCTGATAT TCTTATATTA      840

AAAAATATAT TGCATTTATA ATTTATAAAA TGATTAATAA TGCATAAGCC AAACTATAAA      900

TCTGAAAGAA TTAAGTAGT GTTTGTAAAG GCAAGATAGG AGTGAGATAG TTAATTTAGG       960

TAAGCTGATA TAAGTTTTTC TAGTAAATAG AGTTTCATAT ATGATTAGAG ATATTAAAAA     1020

AACTAAAGCC TACACTGGAA GTTTTAAAGC TTTAATATAT TTTCTATTTC TTTTCTGCAA     1080

GAATTCCAT ATTGAAGAAA ACTAATAGCA TTTTCCATAT ATTTAATGCA TTCAGTAGCA     1140

AGATCTATAG CTCTTTTTGC TAAATCTTGT ATATTGCGTT TGTTAAAATT ACTGCCTAAC    1200

CAGTATGAAT TGCCATTTTC ATTGTTTAAT CTTTTATAAA TAGAATCTGC TAGTTTATCT    1260

CGAGCCACAT CTAGCATATC TTTAGCAGAC CCCCAAGAAT TAGTTGCTTG CTCCATAAAA    1320

GAACGCATTT CTTCTAATTT TACCCATAGT GTGGCTTTGA CAGACTTTAT TTTTCTATTT    1380

AAAGGAGATG TGCTTAGATT AGAAAATAAT AAATCTGACA TTTTTTGATG AAATTCTTTA    1440

AACTCAAGGA GTGTATTGTT TAAGTTATTT TCAGAATTAG CACGATTAAT AAACTGCTCT    1500

GCATTTTTAA TTTCTGAAAG AGATGTTTGC TCATACTCTT CTTGTGCAAA TTCATCTAAT    1560

TTAGCTTTAA TTTCTTCTTC TGAAGGAATA GCAGGAGTTT TACTTGTTGT AGTAAGGCTA    1620

TTTTTAAAAT TACTTTGTTC AATTGGATCA TGTTGTGGAG TAGCTGATTT ATTTTCTTCC    1680

ATCTTTACAT TATTTTGAGC ATGCGAGTCA TTTTGCATTA TTGCTGGACT TGAATTTGGT    1740

AGGGATTCTT TATTATTTGC ACCAGGATCA TCTGACATAT GTTGATTAGA ACCTACTTGT    1800

AAGATTGGAT CATAAGTTTT TTTATTTGAT GATGTAACGT CTTTAGGAGA TTCAATTTCC    1860

TTACTATTTT TATCTACTGA AGTATTAGTA GTATTTTTAT TTTCTTGATG ATCTTTTAAT    1920

GCTAATGCAA ACTGTTCTAT AGATTTTTTA GATAGAAAC CAGAACAACT TTCAAATAAA     1980

AAAAGAGAAC TAAATACTAA ATTAGGTATA ATAAAAATT                            2019
```

(2) INFORMATION FOR SEQ ID NO: 60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1907 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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AGAAAAACAA AATCTATTGC TTCTTCACTA AATCCTATCT TTAAAAATTC ATTTTTTATA          60

CTTTCTATAT TGTATGTTCT GTAAGTCAAA CTATTCATAA AATTTCCATA TTATCCTTTT         120

AATTCTTTAT ATTCTTTCAT AAGTTTTTTA ATTATTTCTT TTCCATCACT AAATAATTTA         180

TCTAACATAA ATCCTGTAAA TTTAGCATTA CTTTTATAAA AATCATAGCT TTCTTGTCTT         240

TTAAGCTGAA ATCTTAAGGG CTTTATCGGG TTTTGTTTTG ATTTTTTTAT TGTTTTGCTC         300

TCTTTATTTC TTAATACAAT TAACGTTTCC AGTATACCAT TTTTTATTAG AAATTCTTCT         360

TGTATAATCC CATCTTCTAT TGCATTAGCA ATTTTTAAGT AATTATAGAC CTGTGCTCTT         420

GCAAGTCTAT AATCTTTAGA AAAAGCTTCA AAACTTTTAT AACCATCAAA CCTATAATAA         480

TGATTGTCTT TAATTTCTTT TAAAATTTTT AAAGTTTCTA ACTTACAATA GATTTCCTTT         540

TTAGAATTAA TTTTTAACTT TTCTTTTAAA GAATTATAAT GATTTAATAC ACTATCAGTA         600

ATAATATAAT TTTCATTATC ACTTAAATCT CTTTTATTAA CCTTAATATC CAATTTAAAC         660

TCCTTTTACA TTAAACTGTC TAATTATTAG ACTTTATATT TTTTTTAAAA AAATTTCTAA         720

AATATTTTCA TATTCTTTTA TATAATCTTT ATTTAAATCA AAATTATTAT TTTCTGCTAT         780

TCGTCTATTT AAGTCTTCTC TTTCAGATAT TGTTCCTAAA AATCTATCTT TTGTTTTTAA         840

TATTTCAAAT AATGTTTTAT GwGTTCTAkT TwwwtTaAAT CTTGTTATTA TCAAAAATAT         900

AGGTAAAAAT AAATTTAATT TTCTTACAAA GAAATTAAAT AAATCTAAAC TTTCCACTGC         960

CCACTTTTCA GCCGTCATTG GAATTATTAC ATAGTCACTA CATAAAGAG CATTTTTTAA        1020

CGTAACATCT AAACTGGGAT TTGTATCGAT TACTATATAG TCATATTTAT AATACAAAGT        1080

TCCCAGGCTG GTTTTTAACA AAAAATCTTT ATGTTCGATT TTATCTTCAC TAAAATTATG        1140

TAGCGTAAGA TAGCTAGGTA TAAGATCAAG ATTATTATCT ACATTATAA TGGTACTATC        1200

GATATCTACA TTTTCTTTCA AAATCTCATA AATATTAAAT TTGGTAAAAT TAATACCTAG        1260

TTTTTCTATT TTTTCGTAAA AATAACTAGT AATAGATGCT TGAGTATCCA TATCAATTAA        1320

AAGAACTTTA TTATTTTTTG ATAATAAAGT AGCCAAAATT ATCGCACTTG TGCTTTTACC        1380

TACACCGCCC TTAATTGACG CTATTGTTAT TATTTTAGGT TTTTTATTAT CCATTTTATT        1440

AGTGGTCCTT GTTCCGGGTA TTTCTTCCCA TAAAATTTAT ATACTTGTTG TTCTAAATCT        1500

GTAAACATAC TAAATAACAC TTTGTTGTAG TGATTGTTTG TTCTTTTTTT ATCTAATAAA        1560

CGATATAATC CCTTGAAATA GCAAAAAACA CTTCCTGCTT TAAATCTAAA TTCCATATAA        1620

TATGCCCTTG CTAATGCATA TGCTTTTCTA GCCCCGTTTA TTTGATACTT TATTAACGGC        1680
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TTTTTAATCG GCTTTCTATA GCCATAAAAA ATACCAATAA ATTTATCTCC TTCTTTAATT 1740

GGGTACAAAT GAGTTTCTTC AACAATTCTT TCTCCATTAA ATAAGGCCCT CAATGATAAT 1800

CTAAATTCGT GTTTTTTCTC ATAAACTCCA AATTTATAAA TATCCATCAT TATTTTTGTA 1860

TGGTACATTG CTTTACCATT TTCTTTTTCA ATTAAAATAA AGCGTTC 1907

(2) INFORMATION FOR SEQ ID NO: 61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1907 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAAAAGATAT ACGTAGAAAT AGAAAGACGT ATTGAAAACC ACAATTTTTT GTTTTACAAA 60

GATGAATCTT TAGTACAACT ACAAGACGCA CTTTCTAGTG CAACAACTTC TTTAAGTGCA 120

CTTACTCAAG GCAATAATGA TAGAGGAAGT GGCATTTTAT CTTCTTTTTT AAGAAAACAA 180

AATTCAAACA ATCATAGTAA AGATATTTCT AATTTACGTA GTCTTAATGA CTCATTGGCA 240

CAGGAACTTG CTAGGTTAAA AAGCAATCTA AATAATGAGG GAATGTTTTA TACAGCTACT 300

CCGAGTGCTA GTTTAGAGGT TATTAAATAC GATCTTAGCT ATTTAAAGGA GGCTTTAGCA 360

TTAATTAAGG CAAAAATTGG TGCAGATACT AAAGAACCCC TAACTAGAAG TTTTAATGAG 420

CAGGCTAAAG GACTAGGGAA TGATGGTAAA GGAGATAGGA GCAATTATTA CGATTTTCTA 480

AAAGGTGTAC AAGAACAAGT TGAGAACTCT TGTAATTTAA AACTTACAAA GTATTTTGGA 540

CTTGATATGA AGTTTAATTC GCTGATTATG TTAAGTGAAG AACAAAAAGT GGAAAGAGAT 600

ATAAAGCTAA TTGAGCTTaC AGTAAATATA ACCAGCTTAT ACAAAGTAGC TCCTTgATAA 660

TGAGGAGTTA GCGATTTaAA AGAGAAATaT TCTCATTTtG AGAAAGGAG TTAAAAAGTG 720

ACTGAGAAAG AAGAAAAAGA AGACCTGCAG GCACmAGATA AAGArGAGCa GCAAaTTAaG 780

GCtGATACTA AAGTTATAAG TGCGCAGGAA TTTGAAGAGT ACATGCGTTT TAAAGAGCAG 840

GCAAATAGTA AATCTAAAGA GACAAGTCGA GATTTAAGTA TAAATGAACG AATAACAAAA 900

GAACTTGCAG AAGTTGAAGA GCGGGAGCGT ATTGAAAAGC AATTGTTACT AGAGGCTGAG 960

CGAATTAATG AAATTGATAC ACTTGCAAAA GCACATCTTA GCAATCATTT TAACAAAGAG 1020

GTGCTACTTG CAAAAGGATA TACATTAAAA GACATTATGC AAGCACAACG TAGAGAACTT 1080

GTACGCAAGT TCGTTCCAAT TGAGCAAATT AAAGCTATTG CCAAAGTATC AGACATAAGT 1140

CATATmGATG GrGAGATATT AGAGCAACTT GTTTCTTTAG CAAAAGTGAA TATTAAATTA 1200

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AGAAAAAATG CGAGTAGCAA TTCTTCTTCT GTTGACTCTA TTAAGGGGAA TATTGCTATT        1260

AAATCAGAAG AAAGAGCAAG TTTGCTTAAT TCTAATTTTG TACCTATTAA TTTCACAGAA        1320

TTTGTACAAG CGATAAGTAA TACTTACAAG CAAAGACGAA TTCAATTTTA TGAAAATCTA        1380

AAAAGACATA AAAGAACAAG TATTGCTTAA AGGAGTTTTT AATGAGCGAT GGTATTACAA        1440

AAATAAAAGA AGAGTTTGAT AAAAAAGTTG CAGAAATTAA AGCATTAATG AAAAATCCTC        1500

AGCAAGATrC TGGTTTGCTT AGTAATTCTr TAGATTTTAG AGATAAAAAT CTAATTTACT        1560

CCAATTCGGA TGGAGTTTTT ACTAGTAGTA AAGACAAAAT AGAAAATTAT CCTGCTAAAG        1620

GGTATCCATA CAAGCGTGGA GTCAAGCTTA GTTTTAGTGC AGATGGTACA ACAGAACTAG        1680

AAGTTGAGGC TGGTGGTGGG GATGACTTGT ACGGAATATG CACTGATATA nATGAGTTTA        1740

CTGGCATGGC AACTGTAGTT CCAATTACAA ATAACTTCAC AGGGTATTTA ACATTTAAnA        1800

AAAATGGACA AAATGGTGTG AATCCGGGTG ATAAGCTGCA TTTTAATGCA CnAGGAGAGC        1860

TTGAAAAGAA TGGGGGAAAT GATAAATCTG TTAATGCTAT AGCnCTT                     1907
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(2) INFORMATION FOR SEQ ID NO: 62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1902 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

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CGGGCATTTA AGCTCTTTTC TACATTGTCT ATTTTGATAT TCAAACCATC TATTTTTAAA         60

TTTAAATTCT TTTCCACATT GTCTATTTTG GCATCTAAAT TAGATATGTC TTTTTGCAAA        120

TTCTTCTCTA TATCAATTAT TTTCTCTTTT AAAAATTCAA AGTTGTAATT ATCATTATGC        180

AGAAAAACAA AATCTATTGC TTCCTtGCTA AACCCTATAT TTAAAAATTC GTTTTTTATA        240

CTTTCTATGT TATATGTTTT GTATGCTAAA TTGTTCATAG ATTATCCTTT TAATTGTTTA        300

TACATTTTTA AAAGTTTACT AATCAAATCT TTTTGATTTT CAAAAATCTC TTGCATCATA        360

AAACTTGTAA ATTTAGCATT GCTTTTGTAA AAATCATAAC TTTCTTGAGT TTTAAGTTGA        420

AATCTCAATG GTTTTATTGA GTTTTGTTTA GATTTTTTCA ATACTGGACT TTCTTTATCT        480

TTCAATACAC TTAATATTAA TCTAAATCCA TTATCTAATA CATATTGTTC CTCAATAACT        540

CCTGCTTCTA TTGCATTGGC AATTTTTAAA TAGTTATACG CTTGAGTTTT TGCAACATCA        600

TAATCCTTTA TAAAAGCATC GAAACTTTTG TATCCATCAA GTTTATAGTA TTCATTATCT        660
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TTAATTTCTT TTAAGATTTT CATACATTCT ACTCTATTAG AAACTCCTTC TCTAAGGTTT   720

ACATACAATT TCTTTTTCAA AGTATTATAA CGATCTGTTT CAACACCATT TTTACTAACA   780

TTAGAAGAAT CTACAAGTAA TGCATTCCCC TCAGAATCAA TATCCCTTTT ATTGATTATT   840

AATTTTGTAT TATTTTTCAT AACAAGCCTC CTTAATTATA AGTTCAACGC GTCGAACTTA   900

TAATTATAAT TATTTTAATT TTGCATAAAA ATTCATTAAT GAATTTTTAT ACTCTTTTAT   960

ATAATCCATT TGAAAATCAA AAGAAGAATT ACTAGCAATT CTTCTATTTA AATCTTCTCT   1020

TTCTGATATC ATTCCTAAAA AATTTTCTTT GGAGTTCAGC ATTTCCAACA ATTGCTTATG   1080

TGTATTATTT TTTTTAAATC TCGTTATTAT AAAATAAGTA GGCAATTCTA CACCTATTTT   1140

TTCCATAAAA AATTTCAAAA GGTCAAAACT TTCAATTGTC CATTTTTCTG CTGTCAAGGG   1200

GACAATTACA TTGTTACAAC AAACTAAAGC ATTAGTTAAA GTAAAATCCA AACTTGGGGG   1260

AGTATCAATT ATAATAAAAT TATATCCAAC ATCTATATGT TTAAGCTCTT TTTTTAATCT   1320

AAATTCATCA AAAGTGTGCT TATAACCAAA AGCATTTATA CTATGTAAAG TCAAATAACT   1380

AGGTATTAAA TCTAAATTAT TCGCTACATT AACGATTGAT CGATTAATAT CTAATTTTTC   1440

TATTAAAACT TCATATATAT TATTTTTTCT TAAATCTATA CTGGATTTTT GTATATCATC   1500

ATAATAATAA CTAGTGGTGG ATGCTTGAGT ATCTATATCT ATTAATAATA CCTTATATTT   1560

TTGAGCCAAT AAGGTTGCAA ATATAATTGC ACTTGTGCTT TTACCAACAC CGCCCTTGAT   1620

TGACGCTATT GTTATTATTT TAGGTTTTTT ATTATCCATT TTATTAACGG TCCTTGTTCC   1680

GGGTATTTTT TCCCATAAAA TTTATACACT TGTTGTTCTA AATCCGTAAA CATACTAAAT   1740

AAAACTTTGT TGTAATGATT ATTTGTTCTT TTTTTATCTA ATAATCGATA TAATCCCTTG   1800

AAATAGCAAA AGACACTTCC GGCTTTAAAT CTAAATTCCA TATAATATGC CCTTGCTAAT   1860

GCATATGCnT TTCTAGCCCC GnTATTTGAA CTTATTAATG GC   1902

(2) INFORMATION FOR SEQ ID NO: 63:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1761 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

AACnGGCCCC GGAAGTTAAA GCCTTGTGGG nCCCATGCtC TAGTGGATGA CCGTTCTTTT   60

AGAGCCTAAA AAGCTATCAT GGGATGAAAC AAGAAGCTAT TTCTATAATC TTTGATTTAG   120

AAATAGCAGT TCACATAAAG ACGCTTGATA TTAATTTAAA TTTAATCTAT AATATAAATG   180

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GCGTAGTATG AATGTAAAAT AATTTACGTT TGAGCTGCCT TATGGAATCA TTTACAATTG    240

AAGGGCTTAA AGAAGTTCTT TAGCAAGAGA GTTTCTTTAA GCCCTAATAA TATTTGAACA    300

ATCTTTTTCT AGGTAAATTG ATCTTCAATA GGATTTTTTA AACGACAGTT GGAATCCGTT    360

TATTCCAATG TCAAAATTGG GTTCAACCCC CGCAAGTGCA ATGCCGAGCC TTTTTTTAAG    420

GTCTGCGTTG TATCTATTAG CAAATTTAAA TGGAATAATA ATTCCAGTTA TGTAGGATGC    480

TACAATTGTG AGCCCTCCTA TTCCTGATAA TACTCCTCCG GTTATTACTG TTGCTGTGCT    540

TTCTGTAACG CCTCCAATAC CTCCTACGAT CATGTGTCCA GCCATTATAA GTATTCCTTC    600

CAAGCACTTG AGAGCCAAGT AGTGCACCAC CACCAATATA ATCTCCTTGA ACAAAGATC    660

CTATCCCTAA AGACAAAAG ATATTCAAAA GTAATGGTGC TAGTATGGTT GCTTTTTCGC    720

TTTCATATTT CATTACAGTC GCGATATCTC CACTCCAACA CCTTTTTCAA GTTTATCTTG    780

TGCAAAGATT TGCATTGTTA AACTAAAAAT TAATATTAAT GTGAAAATTT TTTTCATATT    840

AATATTACCT CCTAATAATT AAGTTTTGAT AAACAAATGT TAGCACAATT TTTAGATTTT    900

ATTTATGGAG TTGAATCTTT TCTTAAAGAT ATTGTTTGAA TTTCTTTGCT GTTCTAAGCA    960

GATTTTAATG TAAAGTTTTC ATTAAACTCT TTTAAATTTG AAATTATGCT ATCTATTTTT   1020

TTTGTATGCC AATTGTATAA TGAATTGTTT TGATGACTTT TTCGAGATGT TCAACTTCTT   1080

TTGAGGGCAT TTCTCTGCCT TTTCTATAAG TTAAGTAACT TTTTAGAGTT TGCCAACTCC   1140

CAATAGTATA GTTATACACC TCTTTGGAAA CATTAATAAA TCTAGAAGTT TGGTTATAGT   1200

AAAGTTCATT TGTTTCTTCT TTATAAAAAA CTTTTTCTAT GATTGAGTTT TGTTTTAGGG   1260

TTTCATCTAA AAATGAAAAA CATTTTCCAA TGTTGATATT TATTGTTGGA ACAACTTTTA   1320

CTAAATGAGA ATTAATGAGA TCTGTTCCAA GTTTGCCAAG TGTTACAAAT ATGTCAGAAT   1380

TATCTACGAA AATAATTTTA GGAAAGTCTA TTTGTAGGTG TTCGTAGAAT CTATCTCGAT   1440

AGATATTTGA ATAAAGAATT GCGTAAATAT AGCCAAGTAT TTCTTCTGCA GTAAATTTTT   1500

TATTGTATTT AACATCAAGA AAATGTCTAA ATTTATTTTT AAAGTTTTCT TTTTTAACTC   1560

TCTCAGGTGT TTCGCTATCT TCTTGTATAT AAAATTGGGAA AACATATCCT AGTGGAATAA   1620

TGCTTAATTC TGATATTTTA GAAGTAACGA AAGCATGAGA AAAACGATCA GTTTTGGATA   1680

GTCTTGTTGT TATTAGTGCT ATATTATTTT GAATTCTAA GATATGTTTC ATTATTTTAT   1740

AACCAGGCCT AATTATGACC C                                            1761
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(2) INFORMATION FOR SEQ ID NO: 64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1717 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

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GCATCATTTC TGAGACTGTT GTTTTTGTAG ATAAAAATTT TCCCAAATAA TATTTAAGCA        60

ATACAAGATT TAGTAAAGCG TATATTTTTA TTTTTTGATT TAATTTCAGT TATTTTTAGG       120

ATTTTTATTA TTTTAATCAT ATTTTCTTTA TCAATATTTA ATGTTAATAA AATTGAAATA       180

ATTTCTTTAC ATAAAAAGTC ACATTTATTG AAATGCTTTA TTACTTGATA CTTTTCTATT       240

TCGTTAATTT TTCTTTCTTC TTTTATATTA TTATTACAAT TCTCCAATTG TACACTACCC       300

ATTTTTGTAT CAGAATTTTT ATTAAAATAG TTGGCAACTC TATTTTGAAA TCTTTTTTCT       360

TTTTTTTCTT TAAAGTGTTG GTTTATCTTA TGGTAACAAT CTTTTTTAGG ATAATTAAGC       420

TTATAATAAA TTTCTGTACC CGAATTTACC CCCATATGTT GATAGTAATT TGTTGTGACT       480

TTTATTTCTT TTTGTAGTCT ATAAATATAC TTTTGCATAG TTCTTAGTGT AGAAATAGTT       540

TGCCCGTTTT TTATAGATTT TCATTGAAAT AATATAATAT GGTTTTTGGG GTATATTTTA       600

GATTTTTGGT ATTTAAATAG CTTGTAGAAA TAAGAACTAT CAATTTATAT TTATATTGGT       660

TATAATTTAG AATATTACTA GATTAATATA TCTAGACTTT ATTTTCTATT TAATATACAA       720

TTAATTAGGA AGCATTATGT GCTCCAAATG GATGATAACC AGATAAAGGG CTTTAAGTGG       780

CTTAAGGAAG ATAAGTTACT TAAAGCCCTT ATCGCATTTA TACTAATTTC CCTAATTTAC       840

GTTTTATTTT GTTTAGAGCG TTATATTATT AATTTTTAAT CATAAAATGG AGGATTAGTT       900

TTGTAATTGT ATATATTTTT AGCTTTAATT GTTCTTTATT AGGCCTTTAA TACTCTAAAG       960

TATTATGCTA TTTCGCAAAA ATAATTTTCT GGATTATATT AGCTTACATA TTAGGATGAG      1020

AATTATAAAT TTTAGTGCAA CAACCTTCTA CAGGGTAAAG GAGTGTATAA AGGCCTCTAA      1080

AGCTTTCATT TTCTTTATTT GTGGAACATT TGAAGATTAC TTTTGGATTT TTTCTAATAT      1140

TTCAAGATAT TCTAACAGGG TTTTAGAATC AACTTCATGT TGATTAGTTT TAGCTAGAGC      1200

CTTATTAAAC TTGCTTCTTA TTAAGGAATA AGCATAATTT TTATTTGCAC TATGGAATAA      1260

TTTTTTATTC ATATGATCTA GTGTTTTGAC AAGAATGATT AACTTATTCT TAGCAAATTA      1320

AATTTGCTTT GTTATTCTTG CCAATGTATT GTTAATTACT CCATCCATAA TGAATTAGCC      1380

CCCTATTATA TTAAATTTAT ATTATAAATA TAGCACAGTA TTTTTTTAAA TTTTTTTAGC      1440

GTAAAACAAT ATATTTCTAA AGTTTTGCAT AAGCTTATTT TATAATGTAT TTATAATTAA      1500

GTAGTAGTGA TTTTTTGTAA AAATTGTTTT AATTCTTCAT AGAATAATAC GTAGTAGTCT      1560
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TTTATTTTTA ATAAAACTCT TtCTAAGGAG CAATTAACTT TATAATAAAT TATAGATTTA   1620

GGATTTTTCT TAAAATAAAG TTTGACTATG ACGGTTATTT CTTTTTCTAA TTTGCGTTTT   1680

ATTTATATAT TTTTTAGTTT TAATTGTTCT TTATTAG   1717

(2) INFORMATION FOR SEQ ID NO: 65:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1566 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGnCACGTAA AATAACTTCA GTTCATATTA TCATATAATA AATAAAACAT TAAGTACAAT   60

AACCTAACAT TTAAAAAGGA TGTACATTTT AATACAGAAA CTGAAGCTGT TCAACTACAA   120

TTATTGCACT TGAAATTTTT TATATTTAAA TAATAATACA AATAATTATA TTAACAAATA   180

TCAATTAAAT TTATTTTTAC ATCATATAAT AGTGCTATAT ATTGTATAAT ATGCTATATA   240

CTTGAAACTA AAGGGGGGGC ATATTAGTTA AGATAATATT CTTATATTTT TTATTAAGGA   300

GACTAATATG AAAAAAATAT CAAGTGCAAT TTTTACAATA ACTTTTCTTG TTCTTATCAA   360

CTGTAAAAGC GATACTAGAA AAGCTATTAA TTCAATACAA ATCCAAAAAT TTACTTCCTT   420

TGATGGGTTG ATTGATGGCT TTCTACGCCT TAATTCAAAT CCCAAAAAAT CTGAGAGGTA   480

AAAGATTGTT TTAACAGCAT GGCTAAAACA TTAAATAAGG CCAAAGACAA ACTTGCTAAA   540

TTCATTAGTG AAAAAGGTGG CAAGACAACC GAAGGAAAGA ATACTGATAC TGCTAAAGAA   600

GATAATAGCA CAGTAAACCC TATTGATGAT GAAATAAGTA AAATTAACGA TATGATGGGA   660

AAAATGATAG ATGCTGCTAA TACCATTGTT GAAAATGTAG CCGAAACCGT AACTGAAGCT   720

aTGGGAGAAG TTGTCGAGGT TAAGAGTATT GGTAATGTAG CAACCAAAGC CGATGTAAAA   780

AGTGTTGTTG AGATTGCTAA AGGAATAAAG AAGATTATTG AAGCTGCTGG TATTGCCGAT   840

AAATTAAAAG CTGAAGCCGA TAAATCTACA AAGCCAATCA GCGAAGAAAG TAACAACAAG   900

TAAGCGGGCA AGATGTTCTC TGGGAAGCAG GGTGATCAAG GTGGTCGAGT TTTCGATGAA   960

GTCATTCCAC CTGAGATTGG AAGAGGAGCT AATCCATTTG ATATTAAAAA GGCTACTAAA   1020

GCTATTGAAA GTGTTAGTGG AGAGCAGATA TTAGGATCTA TTGTTGTGCT GCTACTAAAA   1080

CCGTTAAAAG TGGTGGTGAG GAGCCAAAGG GGAAGAATGC GGATGAAGCT ACAAATCCGA   1140

TTGAAGCTGC CATTGGAGGA AATGACGATT CGGATGCTAC TGCATTCAAG GGGAATATGG   1200

AAAAAGATAA TCAGATTGCT GCTGCTATTG TTTTGAGAGG AATGGCTAAG AACGGGGAAT   1260

TTGCTGTGAA AATGGGTCGA AAACCAAGTG GTGATGGTGA TAATATTAGA GTTCTTGTTA   1320

ATAATGCTGC TAATAAAACT GTTGATGCTT TATCTAAGTT AGCACTAGAA GCTATTAATG   1380

AAAGCTTAAC AAAAATAGCC AAGACTATAC ATTGAAAAAA TAAAGTAAGA ATCAGCATTT   1440

TTAATAAATA ATATTATTTA TTAAAAAATG CTGATTCTTA CTCAACATCT TACGTCAGTA   1500

GTTTACTAAA CTGCATAATC ATTACATATA CACCAACATA TCTAAATTTG CAAACAATCA   1560

TCTTAG   1566

(2) INFORMATION FOR SEQ ID NO: 66:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1552 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CTGTTTTGTA AACCAAAAGT GGATTATAAT AATTGGGCCT ACTAGCTTGA ATTCTAGAGT   60

CAAGCAAACT TACACTAATT GTATCTTGCG GCAATTTTGT ATTCCTCCTT TAAAATTTCA   120

ATTGCTTTTA CACTAGCATT AAATGCTATA GATGCACTGT ATGCATGGTT GCTATATTTT   180

GTGCCTAAAT TAATAAGCCC AACTGTTTGC ATATTAGATA TTGGATAAAT GTAAAAGTTA   240

ACTTTACTAA TATATTCGGG TTGGGATTGA CTTTCTAAAG TATACTTATG GGCTTTATTG   300

TGTAGAAAAT TGCTAAGCAT ACCATAAAGC ATTAACATAC GTGAATTAGC GTCAAAATCT   360

TGAGCGTTTA ACACTATAGC AATAATATAT ATTTGAAAAT TTAAACTGAA TTCCAAAGCA   420

TTTTCATAAA ATGCACCGGC TCTAGAATTA TGATCAAATA GATTTTCTGT ACCATCAAAT   480

TTCAATGCTA TTATATTTGA GCTAGCAGCT GTGATTTTTG AAAGGTACGG GTGATTGTAA   540

GTATTTATGA TATCGCACTC AAAATTATTT TCAGTTGCAT ACGCCTTAAA CCCTTTGAAT   600

ATTTGAGTTA AATGGTTTAA AACCATATCT AAAGTAAAAA TCATTCAAGT GTTACCTTAT   660

AAGTAATCTC GGATAACATT TTGGCTGTAT CAACAAGTGG AATTGCTGCG GTGTTACTAC   720

CCTTTTTAAA CTTACTTTTG ATTGTATTAG CCTTTAAGGC TGGAGAGACT TGTGCTGATA   780

ATAGATAATT TCCATAGTAC CTTATAAAAG CTTGTCCAAT AGCCTCCATT CCCGATTTGG   840

GGTCAAGATT AAACTTAGAA TTTATATAAC TATTATTGAT ATATTCTCTA AATTCAGAAC   900

TACCAGCAAT TTTGGTTAAA TGTTTTCTTG CTGGTAAATT GCTACCCCCT TTTTCATGCA   960

TTCTAGCAAT CCCTGCACGA CCACCAAACC ACCCAATTTC CAATTCCATT TTAAACTCTA   1020

GTTTGTCCAT ATAAACTCCT TTAAAACCAA AGTAAAATAT CCGATTGAAG AGTCAATACT   1080

AAATATTTCA AAGTAAATTA AATCCGAAAT TGATATGCGG TCTTTTAGTT CATAGTTAAG   1140

GTCTTGATAT GTGTAAAGTT TGGAATATCC TTGAATATCA GACATATCAG AGTCATAAAG   1200

CACTGCAAGT TCTTGTGGCC TTATGTCAAT AATAACTCCT GCAAATTCAG TGTACTTATT   1260

TTTATCAAAA ACTCTCTGAT AAGAAGAATC GTTTTCAAGT TTAACAACAG TGCCTTTATA   1320

AAACCTTAAA GGTTGAGGAT CCTTAAATAC GTTGATCATG cGGAAAGACA TATCTGAAAG   1380

TCTTTTTCTA ACACCATTCA TTAGACAACC CCCACACAAG ATGGCGTTGA AGTTTCTCTT   1440

TTTAGTTTTT CTAAAAAgCa TCAAGTTGTG AACAAAAATT CyTGkTTGAG CCACAACCCC   1500

CCTCGsCGGC TTCTTCGGCT CCACTGGCTA CTAGGnTAAT AATCAAGTTC CA   1552

(2) INFORMATION FOR SEQ ID NO: 67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1484 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGTCATTACC GGATTGTAGC TTACATATTC CGCTTTTCTA TCATAATAAT TGATAACTGG   60

TCTTTTAGAA CAACTAGTAT TATAAGTGCG TGTTATGAGT TCATTTTTTG GTTTTATAAA   120

AAACAATTGA GGAATATATC CAAAACCTTT TAGATCCATT CTAGGAAATA ACACTAAAAA   180

ATTATCTGCT CCAAAAAGAG CAAATATTTG GGTTATTACA TCTCTTATTA TTCGAGTAAT   240

TTCCCTGATT TCTTTCTTTT CAATATCATT AATTTTTTCC TTGATTTTTT TCTTTTCAAT   300

ATCATGATTG TTAGTAATTT TATTATTAAT ATCTATTTTG TTAGCTGCAT TGTTAGCAAT   360

TTTTTTGTTA CTTGTCATAA GTAATTACCT TTTACCAAAA TTATGGAGTG TTGTTAGCAT   420

TGTCTTGATT CTCAGCCTGT TCTTGCAGTT TTTTTAAAGc TTCGCCGCCA TCTCCGCCGA   480

ACATTGTAGG TAGAACCGAT TTTAATTTGG CAAAGAAATA ATTAAGATTA AAAATACTTT   540

TAATGCCATT AATTATGGGA TTGATAATAT CTTTGGTAAA ATCAAAATTT TTAATTTTAG   600

CGGTGATCCA GTTAATGATA TTAAGTAATG GGTCCAAAAC AGTAGTGGTC AAATTTGAAA   660

GAGTTTGCTC AGCTGAGGCC AAATTACTTT GAATACTCTC AGCATTATTG ACTTTTTTTG   720

TAAGGCCGAA AGATTTAAAA TCCTCGAACA TTTCCATCAT CTTGGTAATT CTGGAATCTA   780

GATCTACCTC AGCCCCGCCT TGCCAAGCCC TTTTGGCATC TTCTATATAT TTGTCTCCAA   840

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CACCTGACTT CTTTAATAGA TTAAAAAGCT CACTTCCATC ACCCCCAAGA ACACTATTAA      900

CAGCCTTTAC TGCATCTTCG CTGCTCATAG CACCACTGGA TTTAAGCATA GCTGCAAATT      960

CTAyGCGTTT TTCAAATTAG TTTCATTTAA CATATCTArG TCCCTTArAG TACCCTTAAA     1020

GrCACTTGCT TGATTTAAGA ATTCTTCTTT TTCTAGGTCG CGCTCAAATC CCTTCATTCC     1080

GCCAATAATC TTTAAAAGAC TCTCTTTCTC TTTTGGATCA CCATAAAACG CTTTATTGAG     1140

AAGTTGTGTT CTTTTTGTTT TGGTGTCTTC TTCAACCGAT TTTTTAGCAA AACCTAAAAG     1200

GCCTCCTCCA ACTTTACTCA TAGCGTTGCT AATGATATTC CCTAGGGCAC TACCTATAGC     1260

AATTTTGGCA ACAAGTCCTT TTCCTTGAGA GGCCGCTAAC ATTTTACTTT TTGCTTTTGA     1320

TTCTTTTGCA AGTTCTTTAT ACTCAAGACG CCTTTTGTCT CTATCAGACA TTAAAGATCT     1380

TCTGAAAGCC TCTTTTCTAG CTTTCTCAAA CCCCATGCCC TGTTTTATAA GTTTTTTAGT     1440

TTGTGTAAGT CTATATTTCT CAACACGCTG GGTACCGAGC TCnA                     1484
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(2) INFORMATION FOR SEQ ID NO: 68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1452 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

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CTGCTTATTA ATTCCAATAA GTGCTTATAA GTGTTGTTTT TCTTAAAATT AGTTACCATT       60

GGGAAAATCG GTATTTTCAA TTTTAATCTT TTTAGAGCAA ATTCTAATAA TTGCATGCTT      120

TCTACCGACC ATTTTTGAGC AGTCATTGGA ATTATTATAT AATTACTTAC AACTAATACG      180

TTTGTTAAAA TAATTCCCAA ACTAGGACTA GTATCTATTA TTATGTAGTC GTATTTATGT      240

TTTAATAATT TTAAACTATC TTTTAATCTT GTTTCTTTAA ACGGGATGTT ATCGTCATAA      300

AAAAGGTATA AATATATATA ACTGGGCAAT ATGTATAAAT TATTGTTTAA TCTAAAGGTG      360

GAAGAATTTA TGTTTTTTTT ATCTGCTAAT ACTTCGTAAA TGTTTTGTTT TGAAACATCT      420

ACCCCTTGTT CTTCCAAGAG ATCTGAAAAA TAGCTAGTGG TTGATGCTTG TGGATCGGCG      480

TCAATTAGAA GAACTTTATA TTTTTTAGAC AAGAGTGTTG AAAAAATAAT AGCACTTGTG      540

CTTTTGCCAA CACCTCCTTT AATTGAGCAA ATGGCAACTA TTTTAGTGTT TTCTCTATCC      600

ATTTATTTAT AATTCCTCCA TCAGGCAATT CTTTGCAATA AAATTCATAC ACTTTTTTTT      660

CCAATCTGTT TAACATGTCA ATAAATGTTT GAAAATATTT TTTATTAATT TTTTCTTTTT      720

TGATTAACCT AGCAAGACTT CTTAAATAAC AAAACACACT GCCTTTTTTA AATTTAAATT      780
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CTATATAATA TACTTTGGAA AATGTATATG ATTTTAAAGT GCCATTGATT TTGTATTTTA   840

TAACAATGTT TTTTATAGGT TTTCTGTATC CATAGAAAAT TCCTATAAAT TTATCATTTT   900

CTTTTGTAGA GAATAAATTA AGTCCTTCTA ATTTTCCTTG ATTAAATAAT TTTCTAAAAA   960

GAATTAAAAA TTTGTTTTTT TTATATCTGT TTATTTCAAA TTTGTATAGA TCCATTAGCA   1020

TTTTAGTGTG ATATATTGCT CTTTCGTTGA GAATTCTTTT TTTGATGAAA ATTTCTGGCT   1080

TTCTACTTTT TTTTATTATT TCTTTTTTTT TGTTTTTAAG TTTTTCTAGT ACACTTTTCA   1140

TTTCAAACTC TTAATTTATA TAGCTATTTT TATAAATATT TTGTGATTCT ATTAGTTTGA   1200

TAATTTCATT ATAGTATTGA TTATTAAATA TTTTTTTGTA TTCAAGTTTA TTTTGTTTGT   1260

TTAAGTATTC TTTAATTTTC GACCTTAAAT TTGTTGTGTT GGTTTTTCTA TGTAATTGAT   1320

CTAAAAGTAT GTTATATATA TTGGTTTCTA TATTGTCTTT ATGTTTTTGG GGTTCGGTTT   1380

TATTAGTATC GTCCTTTATC TTTTTTATAA TTTGATCGAA ATCCGGGGAT CCTCTAGAGT   1440

CGACCTGCAG GC   1452

(2) INFORMATION FOR SEQ ID NO: 69:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1426 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC   60

TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT   120

TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG   180

CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT   240

TAGCTCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG   300

GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG   360

ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT   420

TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC   480

ATTGGAAAAC GTTCTTCGGG GCGAAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT   540

TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT   600

TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG   660

1053

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AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT      720

TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG      780

CGCACATTTC CCCGAAAAGT GCCACCTGAC GTCTAAGAAA CCATTATTAT CATGACATTA      840

ACCTATAAAA ATAGGCGTAT CACGAGGCCC TTTCGTCTCG CGCGTTTCGG TGATGACGGT      900

GAAAACCTCT GACACATGCA GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC      960

GGGAGCAGAC AAGCCCGTCA GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCTGGCTT     1020

AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC ATATGCGGTG TGAAATACCG     1080

CACAGATGCG TAAGGAGAAA ATACCGCATC AGGCGCCATT CGCCATTCAG GctGCGCAAC     1140

TGTTGGGAAG GGCGATCGGT GCGGGCCTCT TCGCTATTAC GCCAGCTGGC GAAAGGGGGA     1200

TGTGCTGCAA GGCGATTAAG TTGGGTAACG CCAGGGTTTT CCCAGTCACG ACGTTGTAAA     1260

ACGACGGCCA GTGCCAAGCT TGCATGCCTG CAGGTCGACT CTAGAGGATC CCCaGAtGGG     1320

GTTATTATTG TTACTGTTAA TGACTATCTT GCAGAACGTG ATTCCAATTG GATGAAAGCC     1380

GGTTTTTGAA TCTTGTGGGG TGTTAGCGTn GGGGTTGTTC TAATCn                    1426
```

(2) INFORMATION FOR SEQ ID NO: 70:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1425 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
TTTTGGTTGn AATTGCCACn ATAAAAGGGA TTCTTTTTTG GGTTTTATGG GCGGTATTCT       60

TCATTAtAAA nTTmnTCtAT ACAGCAAATA TGGAAAGACT TGAGAGTGCA TTAACCCCAG      120

CAATAAATGC GGCACTCGCT CCATTAAATG AAAAAATCAA TCAATGCATT GACTTAGTTA      180

ATTCTGATGA AAAAAATCTC AAAATATCTA ATGATCTGAA ATTCAATCAG GAAGGAAAAC      240

CTATCTATAA GGAAAGAAyA AATAATGCAA AATAACACTA TTGGTTTAGG ACTTAATTTA      300

CTATCCAGCT TAACTAACAT AGCTAAAACT GATACAAACA TAGATCATAA TTACATTAAT      360

ACTTTTAGTA AAGTAATAGA TTTTTTCTAC AAAACATATA TAAGCACACT AAAATCTATG      420

GAAACAGCTG AGTCAACTAA AATATTTGAA GAAATACAAG ACATTTTAAA ATACAACATT      480

GAGATAATAG AGGCTATCTC TACTGATAAA AGCAAAGAA  TTATCACTTC ACTTAAAGCA      540

ACACGTAACA AAATCATGAA AGAATATATC AAAATACTTA AAAGAGGTGA AAATGCTTAA      600

AAGATTGcAT TGTCTACTAA TTGCTTTGCT GCTATGTTGC ACCACTATTG CTAACCTACC      660
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AGAAGAGCCA AAACCGCCAA TTATTCAAAC ACTAAAATCT TTAGCTAAAT ATGAAACACA     720

ACTTTCAGAG TATGTTATGT ACCTTGTAAC ATTTTTAGCT AAAACAAAAG TCAAAGTTAA     780

TGACCCAAAT TATCCAGAAT ATCCTTATCC AGACTTATCA ACACTAAAAG ACGAACACTC     840

CATAACTGCA GTAAAACACA ATATCAACAT ATATTTAGAG TACATTAAAA AAACAAAACC     900

AATAGCGGAA AAAGTCTATA ATAAATATTC CCAATTAAAA ATGTAAATTA CAAAAAGGTT     960

TTTCTTGCAA GAAATTCTAC TTTATAATTA AATTGGCTTT TACAACAGAA GAAAATCTAG    1020

ATATTAAATT TACTTTAATC TAATATCTAG ATTTTAACAT TTTCAACATG AATATTTACT    1080

AATTAATTAG TGCCcTCTTC GAGGAACTTT ATTACTTTGT CTATCTGTTC TACAGCGTTT    1140

TTAGACATTT TATCCCCATT ACCAGAAGTA TTGCTTcCAA GAAGTGGTAC AGTTACTCCA    1200

ACTAATTTTG CTTCTGACCA TATTTTTCTT TTTGAAATAT CCTGATCCTT GTCAGTAATG    1260

TTTTCAATGG TATTTTTAGC TGCTTTTAAC GCTGCTAATT TGGCCGCTAA TTTATCCTGA    1320

AAGGAATTTT GCAAATTTAA TAGTTTTTCT TTAAGCTCTG CATTGCCTAT ATCTTTTAAA    1380

TTTTCTTTTA ATTCATTTAT TTTGTCTTTA TAATCTTTAA ATTTG                   1425
```

(2) INFORMATION FOR SEQ ID NO: 71:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1423 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```
CAGGTCGACT CTAGAGGATC CCCTAAAATA ATTAACCCTG TCAATAAAGC GAGAGTGGAC      60

ATTGATTGGA TGATCTATTA CAGAAACCCC ATTAATATAC ACCTTTTTAA ATACAATCTC     120

TGTGTTATTT ATAACTTGTA TATTAAAACC TAAATCCATG TATCCGTCGT GATCATACCT     180

CAAAGTAAAA GATCCAAATT TGGTTTTTAA TTTAAGAATT AAACCGAAAT CATATCTATT     240

ACTATCATTT AAAATAACAA CTTCTTCAGA TATTTCACTA GGAAAAATAA ACCTGCTGGG     300

AATTAATAAA AAAGAAATTA ACAATATTAT TACTTTCATA CCTTTTATTA TTATACTATT     360

CTAAAGAAGA AATAAATAGA ATAAAAAATT TTAATTTCTC TTTTTTAAAA CTATTATTTC     420

TAGGTCAAAG ATTATAGAAT AGAAATAGTT TATTGCTTTA TCTAATGATA GCAGCTTATA     480

GGATCTTTTT TAAGATCGGT CTATCATCAA GAATATAAAT CACAAAAGCT TTTTAAAAGC     540

TATCTAAATT CTTTATTCAA GGCAATAATT TATGTAAAAA TAATTAAAAA AACCTCCATT     600
```

TTTGAGCAAA CATTTATACG AATTGATTTG GAAAGTCAAA TGCACAATTC TAACACTGAT   660

TGATAAAAAT ACTTTTTAAG TTTTTTATAT TCAAAATATA AAAAACTTAT TTATAAAAGA   720

TTTTTCAATA TCGATTTTTT TGTGATTTTA TTATTATTGG TATAAAATCA CATAGGGCCT   780

AACCATAAAT ACTCTTAAAG CAAGAATACT TATCTTAAGC CCTATAAATA GACATCGACC   840

AAAGTTAAGG ATGCTTATAG TTAATAGCAC CACTTACCAA GATTATACGC TATTATAGTG   900

TTAAAATCAA TACATTATTC TCAAATAATA TACATATTTA TTTATAAATT ATCTTTTAAA   960

AAATTTACTT CACTTTATTG ATTATTTTTC TAACACTTTC TGATTAAAGT CAATATTTTA   1020

CAAAGTATTT AAATTCGGGT ATTTGATAAA AATAGTGAAT TTAAATACTT TATTTTCCAA   1080

AAACTATAAT TTTATATTCT GCACACAAAA TTATCTATAT TAAATTTTTA ATTATATTTT   1140

TTACACTCCT TATATTCTTT CATAATTTCA TTAAGCAATT CTTCTTTATC TTTAAGTAAT   1200

TTTTCTAGCA AAAAACTAGT AAATCTTGCT TTTGATTGT AATATATGTA TGCATCTTCT   1260

GTTTTAAGCT GAAATCTTAA TGGCCTGATA AAATTTCGAT TGGATTTTTT AACTTTCCCC   1320

CCTTCTTTAT CCTTTAAAAA AAATAAAGAA TTCTGTATAC CGTTTTCGAT TATGTATTTT   1380

TCCTGAACTA ACCCTTCTTC TATTGCATTT GCCATTCTTA AAT   1423

(2) INFORMATION FOR SEQ ID NO: 72:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1405 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TATTTATnAA TATTGAGAAT ATTATCTAAT AAAATATTAA AGATGTAAAA ATTAGTTACA   60

AAAAATTGCT GTAGTGACAT AAATAATAAA ATTGAACTGC TAGAATTTTA TACAAAAAAT   120

AACAAAAACT TTATAAAGTT GATAATTATA AAAAATTTTA AGATTTTCTT GAAAAGTTTA   180

TCATATATAT AAAAAAAGAC AAGCACCATT ATTAATGTTT ATTAGTATAA AACCCCAAAA   240

TAATACAAAT TTAATCCCAA CAATATAGAT AGGATCTTAT TTTTTAGATA AAGTTTTTTA   300

AAACTTTAAA AAATATATTA AAATTTATAA AATATAAAAA GCCTATAATA CCGCACTTTT   360

ATTATCAAAA ATTGCTTATT TAATCTCATA AAAGCATCTT ATTGTTCTAT CAAGCTTATG   420

TATTCTCTAT TATAAGAGCA CAATTAATTA TACCAATTGG GGAGAATATT TTTATGAAAA   480

ACAAAATGAT TTTCTGTATC TGTGTTTTTT TACTTTTAAG CTGCTGTGCT GCAACCATGA   540

CACTGAAACA AAAATTGTTG ATAAAACAAA AACCTAATAT ATTAATGAGA TAAAAATTTA   600

```
ATAGCAGCAA GTAAAGAAAT CATCGAGAAA CGAACACTGC AACAAACTGA GCCAACAGAT          660

CAAGAACCTG TAGATAATAA AAACTGGGAG GAAGTTTTTG ATATAAATAA AAAAACTTAT          720

GACTTTATAA ATAGTTTTTT AACAAATGCT GAGTTCAATA TATTTGCAAC AATATTAAAT          780

AAACCAAAAC AATCACCAAG CAAGATGTTA AATAACATAG CAATTTTAGA GCTTAATCTG          840

GAAGAGACAA TTAATTACTT AGACTCAAAA AAAGATGTCT TAGATAAGGT AAACACCTTA          900

GATTTGGAAA AGATCAAAAA CTCTCTTGAA TAATTACTCT CTATAAGGAA TTTTTTTCAA          960

TAAGCATAAG AAAAACTTTA TTAGATCATC AAAATAATAC CGGTTCTATA AAAAAGGATT         1020

ATTCTAAATT AGATTCTTAT CTTAATACAA TACTTAATCA GTTTAATGAA AAAATTAAAG         1080

AGGTTGGAAA TTTGAAAAAA ATTATATTAT CAATAACTGT TTCAGCATTA TAAATTAAAA         1140

TTTATTAATG CAGGGGCTTA AAGTAAATTA AACCTTTAGA TATAAGGGGC TAATAAACTT         1200

TTTTATTAGC CCCTGTTAAC ATTCCTTTAA TCAAAAATAT TGAATTTTAA TTACAAAAAC         1260

AAAAAAACAA TTAGATTGTG AAAACAATAA AGATCTTATA TAAACAGATA TCAATGAGCT         1320

TAAATCCTAT GTAAGTAAAC TTGCCGATGA TTTAAACAAC TATCTGCAGA AGCAAGAAAT         1380

CTGCATTTAT AGTGTCAACA TATAG                                             1405
```

(2) INFORMATION FOR SEQ ID NO: 73:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1398 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
CnTCAACTTC AGCTCTGTAG TACTATCTGC ACTAAAACTA AGCTTGACTC CACGCTTGTA           60

TGGATACCCT TTAGCAGGAT AATTTTCTAT TTwATCTTTA CTACTAGTAA AAACTCCATC          120

CGAATTGGAG TAAATTAGAT TTTTATCTCT AAAATCTACA GAATTACTAA GCAAACCAGC          180

ATCTTGCTGA GGATTTTTCA TTAATGCTTT AATTTCTGCA ACTTTTTTAT CAAAATCTTC          240

TTTTATTTTT GTAATACCAT CGCTCATTAA AAACTCCTTT AAGCAATACT TGTTCTTTTA          300

TGTCTTTTTA GATTCTCATA AAATTGAGCT CGTCTTTGCT TGTAAGTATT ACTTATCGCT          360

TGTACAAACT CCGTGAAATT AATGGGCACA AAATTAGAAT CAAGCAAACT TGCTCTCTCT          420

TCTGATTTAA CAACAATATT GCCTCTGACA GAGTCAACAG AAGAAGAATT GCTACTCCCA          480

GTTTTTCTTA ATTTAATATT CACTTTTGCT AAAGAAACAA GTTGTTCTAG TATCTCTCCA          540
```

TCGATATGAC TTATATCTGA CGCTTTAGCA ATAGCTTTAA TTTGCTCAAT TGGAACAAAC   600

TTACGAACAA GCTCTCTACG TTGTGCCTGC ATAATGTCTT TTAGGGTGTA TCCTTTTGCA   660

AGTAACACTT CCTTGTTAAA ATGGTTGCTA AGATGCGCTT TTACAAGTGT ATCAATTTCA   720

TTAATTCGCT CAGCCTCTAG TAACAATTGC TTTTCAACAC GCTCTCGATC TTCAACTTCT   780

GCAAGTTCTT TTGTTATTCG CTCATTTATA CTCATCACGC CTTACCTCTT TAGGGGGTTT   840

ACATTGTCTG TTTGCTCTTT AAAGCGCATG TACTCTTCAA ATTCCTGCGC ACTTATAACT   900

TTAGTATCAG CCTTATTTTG CTGCTCTTCT TTATCTTGTG CTTGCAGGTC TTCTTTTTCT   960

TTTTTCTCAG TCATCTTTTA ACTCCTTTTC TCAAAATGAG AATAATTTCT CTTTTAAAAT   1020

CGCTAGCTCC TCATTATCAA AGGmGCTACT TTGTATAAGC TGGTTATATT TACTGTAAAG   1080

CTCAATTAGC TTTATATCTC TTTCCACTTT TTGCTCTTCA CTTAACATAA TCAGAGAATT   1140

AAACTcATAT CAAGCCCGAA ATACTTgTAA GTTTCAAGTT ACAAGCGTTC TCAACTTGTT   1200

CTTGcACACC CTTTAAAAAA TCGTAATAAT TACTCCTATC CCCTTTACCA TCATTTCCTA   1260

GCCCTTTAGC CTGTTCGTTA AAACTTCTGG TTAAGGGCTC TTtAGTATCT GCACCAATTT   1320

TtGCCTtAAT TAATGCTAAA GCCTCCTTTA AGTAACTAAG GTCGTATTTA ATAACCTCTA   1380

AACTAGCACT AGGGGTGG   1398

(2) INFORMATION FOR SEQ ID NO: 74:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1380 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

ATAATAGGCC CAATAAAGAA TATTTTGAAC ATGAATAATT ATTTAATTAC CAATATAAAG   60

CTAAATACAA AATAAATTCA ATATATCTTT AAATTCTAGA AAATTTTTAA TCTAAAAAAA   120

TCATTATTAT AGTGCCCAAA ACAAAATAAA ACTTAAACTG GAAAATTAG TGTTACATAA   180

AATGAATAGG GCTTAAGACA AATTCTTTAT AAAAAACTTG CTTTAAGCCC TATTTCACGA   240

TCATATTGTG ATTCGAATCC GCGTCGAACT ATTTATAGTA TAACAAAAAT TAAATCATAG   300

TCAAGTTGTA TTTTAAATAA ATTTTAATCT TAATTACTAA AACTTTACAA TATAACTAAA   360

ATTGCTATAA GAGTATTTAC TTTTATAGCA ATTTTAGTTA TATTGTAAAG TGATCAATTG   420

TGAGGAGAAA CTTTTATGAA TTCAAAAACA ACAAATAAAA CCACTAGAAA TTGCTATAAT   480

AAAGTTCAAC ACAAATTAAT AGTTCTTATT TCAACAATAT GCTATCTAAA CAAAACACAT   540

AAGAAATATA CACAAAAAAC CATACTCTAT TATTTTAATA AAAATCTAAG AAAAAACGGT   600

CAACCTATTT CTACACTAAG AACTATGCAA AAGTATATTT ATAGACTACA AAAAGAAATA   660

AAAGTCACAA AAAACTACTA ACTATTTCTG ATAACAATAT CGATATCCAA ACCATGTAAT   720

AGAAATCCCA AACACATAGA GCCAGCCCCC CAAAATACAA GGAATTAAAA TCAAGCAACA   780

CATAAACCAT TTCAATAACT TCTAAGTATA AAATGCCAAA GCATAAATTT TGCTATTGCT   840

TAAACTATTT TCGAGTATAC ATCTGTATTA AATTTAAGCT TGTTTTTTCT ATCAATGAAA   900

TCATCTTTTG CATCCTTGTC AAATACAATT TCACTTTAAT TTTAATAAAA AATAAAATAT   960

TTGGACTCAC CAATAGGCTT CAGTGCCCGC ATTAAACCTA AATGTTTAAT TAAAAATTTT   1020

TGGATTGTTA TTCCCAATGC TTTTTCTATC TTGAAAGAAC TTTAAAAGTG CTTTCAAGAT   1080

AGTTTCTTTT TGCACGTTAC TTGAATTTAC ATTCAAATAA TAGGGCAAGT TGCTTTATAT   1140

ATACTCTTTA TTTTTTTTGA TTTTTGTATT TAAGTGTTGA TATTATTAGT AATATTTTAA   1200

ACTTTACTCT TAACTAAAAG CTTGTTTTAT TGTTAAAAAT AAAACACAAA CAATACCCTA   1260

TAAATAGTTT AATATTGCAA TATTATTTAA ACTATAAAAA TATGTAAATA ATAATTTATA   1320

AATTAATAAA AAACATATAA GGGAGCTTTC TTAATGAAAA TCAAAAATAT AGCAACATAT   1380

(2) INFORMATION FOR SEQ ID NO: 75:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1326 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TnAGAGCAnG GATCCAGGAG AAGTTAAAGA TCCTATAATG TATAAATGGT TTTCGCCTGA   60

TCAAATTGAA GATGTTGATC TTCAGATGGG CTACCAAAGA ACTGTAAAGT GGGATGCGTT   120

TTTAAATGCT AATCCTACAA CGATTGCTAA TGAGGTTAAT ACTATTTCAA CTATTGGATT   180

TAGTTCTGAA GTGGTAAGAC TTAATTACTT AAAATTACAG TACAAATTTA GGCACTTAAA   240

GCAGGCGTCT GAAAAATTTT ACACTTCAGA CTCATATCTT GGTGACATTA ATAACAATTT   300

ACTTCCTTTC TCTCAAGCCT ATAAGCTTGC AAGTAGCGAG ATTATTAAAC TTATTAATCA   360

CTTTGTACTA ACAGGCACTG TTTCAATTCA AAAAGATGGA AAAAATCAAA AACGTCTACT   420

TCCCAATATG TATGGACTTC TTAATATGCC ACATCAAGTA AAAGAAGAAG TTGCTAGTGG   480

TGATAAAGAT AAAATGGATA AAATATTTGA AAAAATTGAG GCGGGACTTT CAAAGTTAGA   540

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1059

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GCTAGGAGAC GAATTTTCTA CACCTATGAT GGTAATAGTT GACCCTACAA CTTCGCTCAA        600

ACTCGTAAAG CCATACGCAG CAGCACAGGG TGCAGCAAGT AGCTGCGAAA AATGGGAGGA        660

TGTTTTGATT CAAACTATCA AGGCTATTAA TAATAGAGAA GATGTCTACA TTGAAACTTC        720

AAACTTGCTA AAACATCAAA TACTTATTTA CCCATTAAAC CCAGAGCTTA TTAAGTTTAA        780

ACCTAGCAaG TATATGTTAC CTACACCAAA TGaACAAGTG GATAAAGATT CAACTGATAT        840

TGcTCATTCA TACATTGATT TTGTTTTAGG AGGGTTACTT GCTACTAGAA AAACTATTTT        900

GCAAGTACAT ATCAAACAAA GTTAAAAGTA TAAGGTAAGT GAAAATGAGT GAACAAGAAA        960

ACTTACAAAC ACAAGTTGAG GCTGAAGAAG AACTTTTGGT AACAAAACTT TATTCTGAAG .     1020

TGTTATTGTT ACTAGGAATA GACAAACTTG CATTAAGCAG ACAAAATTTT CTACTTCATT       1080

TATCTTTACT TCAAGCTATT CTAGTAACAC GTGGTATTGA TGCTAGTTCA CTTACATATG       1140

AACAAATATT TTTACTTACC TTTTACCATA TGGGTTGTCA ATTAAGAAAA CAGGGAGTTG       1200

TTCGAGAATT TGAATTTGAT AGGATCAAAA AAGAGAAATT CAATGAACTT GAACTTGATT       1260

ATtATCCTAG TAGCAGTGGA GGCGAAGAAG GTGGCGAGGG GGGTTGTGGC TCAAACAAGA       1320

ATTTTT                                                                 1326
```

(2) INFORMATION FOR SEQ ID NO: 76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1309 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
GGGCTGCTAG ATTAATTGCA GGTAGCAGTT GCTTGATCTG CAAAATTATC TATATTGCCG         60

CCGCTAAAAA ACCCTTGAAC GGTAGTTTTG AAGGTGTTTT TTCCTTCATC ATTTCCATTA        120

CATTTATCAA GTTCAGTCTT TATATGTTCA AGTGCTGATT TAATTTTGCC TTCATCATTT        180

TCTAAGAATT TATCAAATTT TCCAACACCA GTTAAAGCGG TTTTTAACCA GTCAAGTTGT        240

GTTTTTTGAT CATCAGATAG CTTTTCTCTA AGCAGGTCTT CTTTAGATTT AGATTTAGGT        300

TTTTCTTGTG TTGCTTCTTT TTGGGTTAAA TCACGCTTTT GTCTGCTTTT TGTCTGCTTG        360

GTATTTGTAT CATTAGAATT ACAGCCGTTT AGCATTAGTA AAAACAAACA AAATAATATG        420

TTGATAATTT TCATTGTTAC TCCTTTTTTT ATTATTAATA TTCACTTAAC TAAGTATTAA        480

TACTAAATAT GGGATAAACA ATTATTATTT GAATTGATAT GTTTTAAGTG AGGTAGTAGC        540

TATTTAGAAA TGAAAGCAAA TATTAGCCCG GCTATCATTG TGATAGACAT TGCTCCCATG        600
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ATTCCTAATA CCCATTTAAG CATTTCTGAA AGAGACATTA AATTCTTTTC AACATTGTCT    660

ATTTTAGTGT TTAAATTCTT TTCTACAGTA TCTATTTTGG CATTTAAATT CTTTTCCACA    720

TTGTCAATCT TAGTATTAAG TTCGCTTTTA ATAGCATCAA TCTTAACATG TAAATTCTTC    780

TCTACGGCAT CAATCTTGAT GTCTAAATTA GATATAyCCT TTTGTAAATt CTTTTCTACA    840

GTATCTATCT TAGTATCTAA ACTATCTATT TTTAGATTTA AATTCTTTTC CACATTGTCA    900

ATCTTAGTAT TAAGTTCGCT TTTGACACTA TCTATTTTAG AAATAAGATT ATCAAATTTT    960

ATATCaAATT GTTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGCTCATT GTGATAATAT   1020

CTTTTAGATA AATCTTGTGC TATTAGTTGT TCCATGCCCA GCCTAATAAA TTCTTTATAT   1080

ATTTGTTCTT GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTTCCCTT   1140

ATGGTCATAT TATACACTAT TTTAGATTGA TTGGCTTTAG AGATTTTTAT ATGTAAAGGA   1200

GAATTCTTTG CAAGAAAAAC CTTTTTGTAA TTTACATTTT TAACTGGGAA TATTTATTAT   1260

AGACTTTTTC CGCTATTGGT TTTGTTTTTT TAATGTACTC TAAATACTG             1309
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(2) INFORMATION FOR SEQ ID NO: 77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1300 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

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TATCTATATC ACCATTTTTA AAGAATTCTG TAACCACAGT TTTGAAAGTG GTTTTTTGTT     60

GTTCTGCTTG ATCACCATTA CAACTATCAA GTTGAGTTTT TATATGATCA AGTGCTGATT    120

TTATTTTATC ATCATCATTT TCTAAGAATT TGTCAAATTC TCCAGCACCA GTTAAAGCGG    180

GTTTTAACCA GTCAAGATGT GTTTTTTGAT CGTCAGATAG CTTTTCTCTA AGTAGTTCTT    240

CTTTAGATTT TGGTTTTTCT TGTGTTGTTT CTTTTTGGGT TAAATCACGC TTTCCCCGTC    300

TTTTTGTTTG TTGGGCATTG TTTTTTAAAG TGTCATTATC ATTAGAATTA CAGCCGTTTA    360

GCATTAGTAA AAATAAACAA AATAATATGT TGATGATTTT CATTGTTACT CCTTTTTTTA    420

TTATTAATAT TCACTTAACT AAGTATTAAT ACTAAATATT GGATAAACAA TTATtATTtG    480

AATTGATATT CTTTAAGTGA GGTAGTAGCT ATTTAGAAAw rAAAGCAAAT ATTAGCCCGG    540

CTATCATTGT GATAGACATT GCCCCCATAA TTCCCAATAC CCATTTAAGC ATTTCTGAAA    600

GAGACATTAA ATTCTTTTCA ACATTGTCTA TTTTGGCATT TAAATTCTTT TCTACAGTAT    660
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1061

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CTATTTTGGC ATTTAAATTC TTCTCTACAT TATCAATCTT AGTATCTAAA TTAGATATAT    720

CTTTTTGTAA ATTCTTCTCT ACATTATCAA TCTTAGTATC TAAATTAGAT ATATCTTTTT    780

GTAAATTCTT CTCTACATTA TCAATCTTAG TATCTAAATT AGATATATCT TTTTGTAAAT    840

TCTTTTCTAC ATTATCTATC TTGGTATTAA GTTCACTTTT AACAGCATCA ATCTTAACAT    900

TTAAATTCTT TTCTACAGTA TCTATTTTAG AAACAAGATT ATCAAATTTT ATATCAAATT    960

GTTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGTTCATT GTGATAATAT CTTTTAgATA   1020

AATCTTGTGC TATTAATTGT TCCATGCCCA GTCTAATAAA TTCTTTATAT ATTTGTTCTT   1080

GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTTCCCTT ATGGTCATAT   1140

TATATACTAT TTTAGATTAA TTGGCTTtAG AGATTTTTAT ATGTAAAGTA rAATTTCTTG   1200

CAAGAAAAAc CTTTTTGTAA TTTACATTTT TAACTTCAGA TATCAGTTTT AAATTTTTTA   1260

CTGTAgATTT TTTACAAAAA CAGTATTGCA AAAACTCTnA                         1300
```

(2) INFORMATION FOR SEQ ID NO: 78:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1295 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```
GAATTAATAA GCAGAGATGA TAATTTTTTA GGCGTTATTC ATGAACGTGA AGACTTGAAC     60

AAAAGGATAG CAGAAAACGA TACTTtCGAT TTAAATAAAG ATTaTATAAA AGAATATGaA    120

ATTACACTTG aAAAATTTTT TCAGTTGTCA AAAAAATTTT TAATTTCATA ATATATAGGG    180

AAATGAAATG AGTGTAAAAT TAAAACATAT GAATATAAAA ATAAAGATc GTATTAATAC    240

TGGcAAAAAT CAAAAGCAAA TTGaAATTAA TTGTGATGAA GaTAAAATGG AACGATTTCT    300

ATTTTTAAAA GAAAGGCTAA TAATCAACTT CCAAAAAGAA ATTCACAATA AAATAGAAAC    360

AATGAAGATC TTAAAAGAGA TTAAAGATAA AGAATATTAT AAATTAGATG GCTATCAAAA    420

CTTTGAAATG TTTACTAGGA ATTACAAAAT AGCAAAAAGC CAGGCTTATG AATATTTAAG    480

AATrGCAAAT GCAATAGAAG AAGGryTAGy TyrGGArAAA krCATAATCG AAAACGGTAT    540

AyAGAATTCT TTATTTTTTT TAAAGGATAA AGAAGGGGrG AAgTTAAAAA ATCCAATCGA    600

AATTTTATCA GGCCATTAAG ATTTCAGCTT AAAACAGAAG ATGCATACAT ATATTACAAA    660

TCAAAAkCAA GATTTACTAG TTTTTTGCTA GAAAAATTAC TTAAAGATAA AGAAGAATTG    720

CTTAATGAAA TTATGAAAGA ATATAAGGAG TGTAAAAAAT ATAATTAAAA ATTTAGTATA    780
```

GATAATTTTG TGTTAAGAAT ATTAACCTAT GTGATTTATC AAATATATTA TTTAGATAAG   840

GTATTTGATA AAAAACAGGG AATTTCTTTG TTTATAAAGT AGTTATTTAA ATCATAAAAT   900

GTCAAAAAAA TCGGGGTAGT AAAGTAAAAA GTAAAGATG ATTTACAAAT AAATATGCAT   960

ATTATTTGAG AATAATGTAT TGATTTTAAC ACCAACAAAA TTCATTTTCC AAATGATATA   1020

AAAGTTTTTA TAAATGAGCT TATAGGGTCG TTTTCAAAAT TAGGCTATTA TAAAGAGGCA   1080

AAAGAAACTT TGCAAAATAT TTTTTGTATA TTAGATAGTA ATTAAAAATG ATTTAGTCTA   1140

CTCAATAATT TATATGAGAT AATAAAGTAT ATTAAGGATA TGTGCTTTAT TAATAAAAAT   1200

AAAAATAAAA ATAAAAATAA AAATAATTAT ATCTTAATAA AAAAATTGGA AATACCGCAA   1260

TTATTGATAA TTTATCGAAT TTAGATACTA ATATA   1295

(2) INFORMATION FOR SEQ ID NO: 79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1284 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TATCnTTTTT CCTCAAAAGT TTAATTGGAA AATAAAAAGT TATnCTCTGG TGATATTAAT   60

AATTTTATTA TTGGGAATTC ACAACGCTCA GTTGAAGTTA ATGTTTTGGG ACAATTTGAA   120

AAGCTATGTA AACTTCTTAA AATTCCTTAT ATCCCAAGAC ATACAAATAA yTCATATATA   180

TTAATTGATT CACTtCGTAT TAATCTATAT GGAGGAGATA AGGCAAGTGA TTTTGAAAGA   240

TTTAGAGGCA GTAATTCGGC ACTTATTTTT GTTAATGAGG CTACTACTTT ACACAAGCAA   300

ACTTTAGAGG AGGTCTTAAA AAGACTTAGG TGCGGACAAG AAACTATTAT TTTTGATACT   360

AATCCTGATC ATCCAGAACA CTATTTTAAA ACCGATTATA TTGATAATAT AGCGACATTT   420

AAGACATATA ATTTTACAAC TTATGATAAT GTGCTACTTA GTAAAGGATT TATCGAAACA   480

CAAGAAAAAC TCTATAAAGA TATACCATCA TATAAaGCAA GAGTTTTGCT AGGTGAGTGG   540

ATAGCAAGCA CCGATTCAAT TTTTACACAA ATAAATATTA CTAATGATTA TGTATTTACT   600

AGCCCGATAG CATATTTAGA CCCAGCATTT AGTGTTGGmG GGGATAACAC TGCATTATGT   660

GTTATGGAGC GrGTTGATGA TAAGTATTAT GCTTTTGTAT TTCAAGACCA ACGACCAGCC   720

AATGACCCGT ATATTATGAA TATGGTTAAG ACCGTTTTAG AAAATTTTAA TGTACATACA   780

yTTTATTTAG AAGATAGAGA CAATACAAAA GGTGCTGGTG GATTGACyCG yGAATACATs   840

TTGCTAAGAA ATAATATGGG TCAATATTTT AGAATTGTTC CAGTTAAGCC AAAGTCTAAT   900

AAATTTAGCA GAATAACArC GTTAATTACG CCGTTTAyTT ATAAGAAACT kTACATTACr   960

AAGTACAGCA GTTCTTCTGT ATTTAATGAT ATTTATTCGT ATAAAGGAGA TAACAAAACC   1020

CATGATGATG CTCTTGATGC AATATCTGCA GCATATTTGA TGTTGTCTTT AGGGTATAGA   1080

GAGAGAAGTG TTCACTTTGG CAATCAAAGA TTTTTGTAAA TTTTATTGAC AAAAATAATA   1140

GTTTTTGCTA TCATACATCT AATTTAATAA AGAGAAATAA AAGGTGTGTG ATTTAAGAAA   1200

AACAAAATTA ATAGATAAGA TAAGTTCACT AGAACTATAT AAATACTCAA TATTTTTTAG   1260

GAATTATATA GAAAATGTAG CAGA   1284

(2) INFORMATION FOR SEQ ID NO: 80:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1271 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GCTTGAAAAA TTTCTTTCGG GGCGCTTAAT GGAAGAATCA TTTCTTATTA GAATGTGGTT   60

AACTATTTTA AATTTTTTTC AGAAAGAATA AAAGCAAAGA AGAATATATA TAAAGCTTAT   120

GTTATAAAAA ACCTGGAAAA TCAAATTAAT GAAATGTTGT AAAAATCCAG TAATAGATTT   180

TAAGAAGAGA ATGTTTGCAT GTTGGTTTTG TGGAAATGTT TTTTAGTGTT TGCCGATATT   240

CAATGGAATT GAAAGAATTT TTTAGGAAAT TAGAAAAAGG TGGTATTGTT GTTGAGCAAA   300

CTATTTTAGA AATTATTCAA AGCAAAGTTC TTAACTCTAA GAACAATTTG GAAGAATTTT   360

TTAGATGAAG GTGAATATGA GCTTTTTTTA AAAAAAGAAA AAACCCAAAA CGAATTTAGA   420

AGAATCTCTT AAGGGTCAAG ATAAATGAAT ATATTAATTC TATTCCATCT AGTACTTACA   480

AAATCGTCTC GGATATGTTT GAGTTTTATT ATGTTTTTAA TAGTTTGGCG TTTTTCCCTT   540

ACAAATCTTT TTTTTCATTT TTTAATGTAG ACCTTTTAGA TAGTGCTGAG AATATTAGCA   600

TTGTTGACTT TGAAGGTTGG ATTTGGGGGG AATCCTCTAG AAGTCGACCT GCAGGCATGC   660

AAGCTTGGCA CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCC   720

AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG GCGTAATAGC GAAGAGGCCC   780

GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGCGC CTGATGCGGT   840

ATTTTCTCCT TACGCATCTG TGCGGTATTT CACACCGCAT ATGGTGCACT CTCAGTACAA   900

TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC GCTGACGCGC   960

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CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC GTCTCCGGGA     1020

GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGAGACGA AAGGGCCTCG     1080

TGATACGCCT ATTTTTATAG GTTAATGTCA TGATAATAAT GGTTTCTTAG ACGTCAGGTG     1140

GCACTTTTCG GGGAAATGTG CGCGGAACCC CTATTTGTTT ATTTTTCTAA ATACATTCAA     1200

ATATGTATCC GCTCATGAGA CAATAACCCT GATAAATGCT TCAATAATAT TGAAAAAGGA     1260

AGAATATGAA T                                                         1271
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(2) INFORMATION FOR SEQ ID NO: 81:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1269 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

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GAATTTTTCA AAATTACAAA ACTTTAACCC AAAATGGTAA AACTTTAATT TTTTGTAATT       60

TTTACATAAA AGTGTTAACT TTAAAATyCC AAACTTTATA ATTTTGGAAA ATTATCAATA      120

CTTTTTTAAT TTATTCTTTA TTTTCAAAAT AATCTTTATA TACTTATATA TTATGTATAA      180

GTCTGTAAAA GAACAACAAG AAAAAGGAAT AGATCATACA TGCAGAATAC TTATTCTTAC      240

CGAAACAATA TTTGAAATAA ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA      300

AAAGTATAAC GAAAATCTCA AAAACAAAAA TCTACCTCCT AGTAATATAT CAACAATGAA      360

AAAATACTTA AATCAATTAG AAAAAGAAAT AAAAATCATA GCAAAATTCT ATTTTAAAAA      420

CGATCAATCT CTAATTTATT ATAAACTTAA TTATACCCTA GAAAAAATTT GGTTAAAACT      480

AATAGAATTA TTCTACAAAG AATTAAAACA ATTTATACAA AAGAACACTA CTACTTAATT      540

GTAAATACAT TATAAAATAA TCTTATTCAA AACTTTAGAA ATATATTGTT TTACGCTAAA      600

AAAATTTAAA AAATACTGTG CCATATTTGT AATATAAATT TAATATAATA GGGGGCTAAT      660

TCATTATGGA TGGAGTAaTT AACGATACAT TGGTCGCAAG AATGAAAAAG CAAATTAAAT      720

TTAATAAGAA TAAGTTAATC ATTCTTGTCA AAACACTAGA TCATATGAAT AAAGAATTAC      780

TTTATAGTGC AAATAAAACT TACAATTATG TCTTAATACA AAACAATTTT AATGAGGCTC      840

TAGCTAAAAC TTATCAACTT AGGGTTAATT ATAAAACCCT ATTAGAATAT CTTGAAATAT      900

TAGAAAAAAA TCCAAAGTA ATCTTAAAAC GTCCCACAAA TAAAGAAAAT GAAAGCTTTA      960

TAGGCCTTTA TACACTCCTT TACCCTTTAG AAGATTGTTG CACTAAAATT TATAATTCTC     1020
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1065

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ATCCTAATAT TTAAGCTAAT ATAATCCAGA AAATTATTTT TGCGAAATAG CATAATGCTT      1080

TAGAGTATTA AAGGCCTAAT AAAGAACAAT TAAAACTAAA AAATATATAA ATAAACCGTA      1140

AATTAGGAAA ATTAATGTTA CACCAAATGA ATAGGGCTTA AAACAATTTC CTTTAAAGAA      1200

ATTTCTCTAA GCCCTACTTC ATTGCTTATT ATTACGTCAA TTCGAGCATA AAGCCGAACT      1260

AATTTATAG                                                             1269
```

(2) INFORMATION FOR SEQ ID NO: 82:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1225 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```
CGGCCTTTTT TGTTGCAGCA TGATCAAGAA TCCCTTTAAA TTTAATGGTG AATTTGTCGC        60

TCACTAAGCC CTCACTTGCT TAAAATTAAT TCATACAATT CTTTTTCTAA TTTAATCTCA       120

GCAAGTCTAT TGACCTCTAA AgCTCGTCAT AAGGCAATTT CTTTACATTG TCGTACGAGC       180

AAaTATTCAT AATTACTGGA AAATAATATT TGTCGTTCTT AATCTCGTCA AGCAgTTAAA       240

ATATTTTTTT CTAGTCTCAT TAaGACTTGC AATAGCTTTA TCAATATCTC TATCTCTTTT       300

GCTCATTTAG CAACCAGCTC ATTGGAATTT GATGTACTTG ATGAAAGTGA AGTGGCTACT       360

TTTTCATAAT CAAAATTTTC ATTAATATAG TCAAAAGCAA CAAAATCACC AACATTATTT       420

TCATACTCAC TCAAATATAC TAAAGCGGGC TTTTTTAGAT CATTGTCTAA ATGAAAAGTA       480

TTAAATTGTG CAGTGTAAAT TATTGCAACA AGATAGTCCT TATAATAAGA AATAAATTCT       540

CTATTTTGAT CCAAAATCAC ATAGAATTCG TCTAAAAATT TTGGACTTAT CATTAAGCTT       600

GTGATTTCTC TTAAGTATTT AACCTCATTA AGCTTTAAAA CAGCGTCACT TTGATTAAAT       660

CCTAGCACCT TTATCCCATT CATAGACTGG TAATACTTTT AGTGGATATT CATAAGTTTT       720

ATTTTTAGTT AAAATTTTCA TTTTATATCT CATTATCATA ATAAGACTCT CCTTTTAAGT       780

GTTGTTTGGT TTAGTTTTTT GGCAATTAAT AGCCCTAATT TCAAAGATA CTTTTTCGGC        840

CTCAGCAGAA TAACTTCTTG AAGGCTCTTC AGTAAAAATT GCATAGTTAG AAATAATTTT       900

GGTAGCAATT CTATCATTGA ATACTAAATC AAGCATTTTA TCCTCTTTTC TCACATCCAT       960

GTTGTAAAAC TGTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC TACCTAGTGT      1020

CACTTCAATG TTGAAAACAT AAGTTATTGT TTTGGGATCT CTTAAGCTTA TTACAGGCAT      1080

ACCTTTATCT TCACTACTAA TCACTGCTCT TGTTGTAGGT TCGCTTGTAA GCTCTAGCTT      1140
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GCCACTATGT AACTGCGGTA CCACCAATTG AAAAATAAAC TTCTCTTAAA TCATAAAATT   1200

GCATTTTTAG ACCCCCTTTT TAGCA   1225

(2) INFORMATION FOR SEQ ID NO: 83:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1200 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGGCTGGTGC TGTTAGTGCT GTTAGTGGGG AGCAGATATT AAGTGCGATT GTTAAGGCTG   60

CTGGTGCGGC TGCTGGTGAT CAGGAGGGmA AGAAGCCTGG GGATGCTAAA AATCCGATTG   120

CTGCTGCTAT TGGGAAGGGT GATGCGGAGA ATGGTGCGGA GTTTAATCAT GATGGGATGA   180

AGAAGGATGA TCAGATTGCT GCTGCTATTG CTTTGAGGGG GATGGCTAAG GATGGAAAGT   240

TTGCTGTGAA GAGTGGTGGT GGTGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG   300

CTGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGTA   360

CTGATGCAAT TGGAGAAGTT GTGGCTAATG CTGGTGCTGC AAAGGTTGCT GATAAGGCGA   420

GTGTGACGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTGAAA   480

AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA GTAATAAAGG GGCAGGGAAG TTGTTTGGGA   540

AGGCTGGTGC TGGTGCTAAT GCTGGGGACA GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG   600

TTAGTGCTGT TAGTGGGGAG CAGATATTAA GTGCGATTGT TAAGGCTGCT GATGCGGCTG   660

ATCAGGAGGG AAAGAAGCCT GGGGATGCTA CAAATCCGAT TGCTGCTGCT ATTGGGAAGG   720

GTAATGAGGA GAATGGTGCG GAGTTTAAGG ATGAGATGAA GAAGGATGAT CAGATTGCTG   780

CTGCTATTGC TTTGAGGGGG ATGGCTAAGG ATGGAAAGTT TGCTGTGAAG GATGGTGGTG   840

AGAAAGGGAA GGCTGAGGGG GCTATTAAGG GAGCTGCTGA GTTGTTGGAT AAGCTGGTAA   900

AAGCTGTAAA GACAGCTGAG GGGGCTTCAA GTGGTACTGA TGCAATTGGA GAAGTTGTGG   960

ATAATGCTGC GAAGGCTGCT GATAAGGCGA GTGTGACGGG GATTGCTAAG GGGATAAAGG   1020

AGATTGTTGA AGCTGCTGGG GGGAGTGAAA AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA   1080

ATAATAAAGA GGCAGGGAAG TTGTTTGGGA AGGCTGGTGC TGATGCTAAT GGGGACAGTG   1140

AGGCTGCTAG CAAGGCGGCT GGTGCTGTTA GTGCTGTTAG TGGGGAGCAG ATATTAAGTG   1200

(2) INFORMATION FOR SEQ ID NO: 84:

1067

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1182 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

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GCTACAGAAA TAAAATTTTT AACAACAATT ATTTTATTA  TTTCGGCCTT TTTTCTCAAA        60

TTTTTATTGT CCCAAAAAGG TAACAATAAA ACGAATAACC TAGAAGAGGT GGCCAATTTG       120

TTATTTAAAA ACTTTAAAAT TTTTTGCAAT GCATTTTAAA TTCCAAATTA CTTTTGCATA       180

AATAAATAAA CTTCTCTTTG CGCAAATGGA AATCCAAACC GATCACTAAA ATATTTCTTA       240

AAAAATTATA TTCAGCTAGC CCAGATATCA TTTGCTTTTC ACACTGAAAA GCATCCTCTT       300

GAACACTAGA ATTAAAAACA CACTGTTTTT AAAATTTTCA ATTTAAATTA AAGATTGTAT       360

TTTGGCAAAA AATTTTCTAT ATCTATTTTA TATTCTCTGT CTTCATTAGA AATTAACATA       420

ATCTTTAATC GTTTTAATTT TTTGATTTTC TTAAAAAACC CTTTAGAAAT AGTAACACAC       480

AAGGTATTTT TTACTACAAA AGGAAATTCT AAATGAAAAA ACTTTTCATT TATATTCGGA       540

TCACCAATGT TAAAATCTTT TAATTGCTGC CATTTCTCAC TTGGTAAATT ATTTTCATGC       600

TTTGAAACTT TAGCATCTTC AAATCCTTCA AAAATTACAC TTTTAAAACC TAAAATTTTA       660

TTGTCATGCA CTTTAAAATC AAACCTATAA ACGGTAGATA ACGCTTTATA AGCATCTGCA       720

CGATAACCTG TCGCTTTTAT CATCTTTTTA TGCTTAAGCT CAGGAATTAT AAGCTGTGAT       780

TTTATAAAAA CCAATTCTTT CAAATTACTA TCTTTAAAAA GATATGTATA GGTTTCATCA       840

ACAAAAACAT TATCATCAAA CTTTTCAACA ATTTTATTAT AAATAACATT GTTTTCTTTT       900

TGTTTGTAAA AAAAGAAACC TAAAAAAATA CAAATTAATA GTAACCCAAA AAATAATATT       960

TTACCCATTA ATAATCTATC CTACTTATGA AAAATCATAT CAAATGCACT ATAAAAATGT      1020

GAGCTATTTT CCCTGCTTAC CCTGAAAGAA TATTTTTTTT CTCATTATTT ATCTCATCAA      1080

AACATTCAAC ATATACATCA ATTCCATTTT CTTCTGGCGA ACTTTCTTAT TTTATTCCAT      1140

TTTTTCACTG GAAATCCAAG GAAACTCATA TCCAAAATTT AA                         1182
```

(2) INFORMATION FOR SEQ ID NO: 85:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GnACnAGGAA CCGGCACTGA CGAGTCATTT AGACTGATTT TCAAGACCTT TTTAAATGTA   60

GACATTGAAG TTACTACTCC TGAAGCTGGG GTTATTGATA TCTCTTTAAA AGGGGTAATA   120

AAAACAAACT TTACTACATT TATTTCGCCT AGCACTAAGA AAGGAAAACG ACTAAAAAAG   180

ATAATTCTTA GAGAAAAGAA GCCGGGATAC GCTGCATCTA AAAAAGCTTT AGTATTTAAC   240

TCACTTCCTA AaGGCTAtGA TCATTCAATT TATGCTTTTA TTAAGAGAAT TATTCCTATT   300

GGTAGAGTTC TCAAAATTAA TAATACAGAT GGTAACAATA TTATTACTTT CAATAACTAA   360

GGAGGTTTTA TGGCTGATGA TCAAGAAAAA TTACTGATTG ATGAAGAAGA AACGGTTCAA   420

ATTAAAGATT TAAATAAGGT TACGACCGTT AACAATACTG ATCTTTTACT GCTTGATGAT   480

GGAGCTGCAA GCAGCAATGC TATCACCTTT AAAAACTTCT TAAAAACCGT TAATCACCAA   540

ACATTTAAAG GCGAAGAGCT AGGCTATTTT AAAGAGATAA TTAAATCTAC AATCGCTACT   600

GAACTTGCAG CTGATAAAGA TTTTATAAAA AGCATTTACG ATTTAATCGT TGACAAGCTA   660

ATTGAGAATG AATCTAGTAA ACTTTCAAAT CTTTTTAGTA AAATCAAATC GCGCCTTACA   720

GATAGCATAT CATCAGCCAC TTTATCTAGA AGTGATGATC TTTTGATAAT GCCTTCATCA   780

GATACTATTC AAAAAACACC CGTTCCTAAA CATATACTTG GAGTACCATC AAATTTTACT   840

TATGGCAGCA TAACTAGAAG TACTACACTT TATCCTTCTG ACTATGAGAA TAAAGCGATA   900

TCTATTAATA TGGAAGACAA TGATGATGTA ACTCTTATTT TTTACAAAAA TTACGATAAT   960

GATCCCATTT ATCTGGATAT TGAGATTCAA GTAAAAATCA ATGGATAATA GGATGCAGAA   1020

AAAATCATTA AAACTTATGT nTTCTGATGA AATTACATAC AATTGGGTTT ATGAAATACG   1080

GGCCCTCGCG GACTATTCAC CAGAACTCCC ATTATAACGG AnGGTATATC CAAAAAAGAG   1140

CCTCCTGTAT GGAGATCGTC CCGATCTTTA AAACTGTA   1178

(2) INFORMATION FOR SEQ ID NO: 86:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1177 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATATGTATA ACAAAAATTA TTTTTGTCAG GCTTTTTACA GAAATTATTA TAATAAATAA   60

AAGCTTTATT AAATTCTCAT GTTAAAGAGC TTAAGAAAGC CGCTGGCTTA GCTCAATTTA   120

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TTTTAGATAA ACTCACTAAA CAATTAAATT CAGTTCAATT TAGAATTAAA ATTATTTTGT      180

ATTTGTTAAA ATAAAAGAAC CTATTTAAAT TCTCTTGTTA AAAAATTCAA ATAAGTTCTA      240

CTTTAAAGCT ATATACTAAC TTATTACTTT ATAAAATTTT AATCATTCTT AATTTAAAAA      300

ATGCTTATTG AATATAGAAT AAATAATTGG AGCAAGCGTT ATTCCCATTA TTAAAATTAC      360

TTGTATTGTT CTATTACTTG CAGTAAGTTC GTTTTTTAAA ACATTTATTT TATTATCTAG      420

GCTAAATATA TCCyTTtGTA AGGTTTTTTC TACACTATCT ATTTTAGtAT TCAAGCTaGA      480

TATATCTTTT TGCAAAGTTT TTTCTACATT ATCTATCTTA GTATCTAAAC TATCTATTTT      540

AGAATTTAAA TTCTTCTCTA CACCATCTAT TTTGGCATTT AAATTCTTCT CTACAGTATC      600

AATCTTAACG TCTAAATTGG ATATATCTTT TTGTAAATTC TTTTCTACGC TATCAATCTT      660

AAAAATAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA      720

TGTTAGCTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAGTT GTTCCATACC      780

CAGTCTAATA AATTCTTTAT ATATTTGTTC TTGAGTTACA CTTGCAATAT TTGTTGACAC      840

TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT      900

AGAGATTTTT ATATGTAAAA TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTTACATT      960

TTTAACTGGG AATATTTATT ATAGACTTTT TCCGCTATtG GTTTTGTTTT TTTAATGTAC     1020

TCTAAATATA TGTTAATATT ATGTCTTACC GCAGTTATGG AGTGnTCGTC TTTTAGnGTT     1080

GATAAGTCTG GATAAGGATA TCnGGATAAT TGGATCATTA ACTTTAACTT TTGGTTTAGC     1140

CAAAAAnGnT ACCAGGnACA TAACATACTC TGAAAGT                              1177
```

(2) INFORMATION FOR SEQ ID NO: 87:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1137 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
TCACGnCCAT GTtGtAAAAC TGTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC       60

TACCTAATGT CACTTCAATG TTAAAAACAt AAgTTATCGT TTTGGGATCT CTTAAGCTTA      120

TTACAGGCAT ACCTTTATCT TCACTACTAA TTACTGCTCT TGTTGTAGGT TCGCTTGTAA      180

GCTCTAGTTT GCCACTATGT AGCTGTGTAC CACCAATTGA AAAATAAACT TCTCTTAAAT      240

CATAAAATTG CATTTTAGCC CCCCTTTTAA GCACTTAAGC TGTTTTGATA ATCAACTATA      300

TCTTGAGTAG TGATTACTAA AGCAACAGCA TTAATGCTAA AGTTATAAGT AATATTCACA      360
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CTAAGTTCTA ATTTAAGTTG TGGTGTAGGA GAAAGGGTAA GGTTTAAGTT TTTATACTCT 420

ATAATCAATC CCCTGTCGAC AAACCTTTTA AGAAGACATT CAATTGCTGA AGTATATGCA 480

TTGTCTCTAG CACCACTAAG TTGTAGTGCA GATAATTTGC TATTTTGCCT ATTGTTTTTG 540

TTCCAAATTC TAATAAGCTC AATAATCGCT TCATTTTTA TATAATGATA AGTGAAAAGC 600

TCGTCTATTG AACTTCCAGC AAGATCAACG CTCTCTTTAA AGGCAGGCAT ACCATCAAGA 660

CCAGTTTCAT TAAGAAGTGA ATAAAGTTG ATTTTTGCAG TTCGCAACTT TCCAATTACA 720

GTATCATCAA CAAGTGGTGT AGCAGCCAGC GGCATGCCAT AAGGATTTAC AGCATGAAAA 780

ATACTAGCCT GATGTAAATA TTGACTTATA AATTTGAGGT GTAAATTGTC TTTATTATTA 840

CTGTAAACAG CAATATTTCT TTCTTTTTCA GTATTGCCTT TATCTTTAAA TAGTTCTTTT 900

ATTTCTTGTT CTTTAGTCGA GAATACAAAA AAAATTGAAG GTGTTTTAAA CTTATCATAA 960

TCATCTTTAT AAATCTTAAG TCCATCATCG GAATTATCAC CCTCAGTATT AATAAGTACA 1020

ACAAAAGTGT GTCTATGTAC TTTAAGATAT TTTTTTAACT CTTCGGGTTT ATCCTTATAA 1080

ATAAAAAGAA CAGCGGATTT TAATGATTCT TCACTTGAAT TGAAAAAATT TGACATT 1137

(2) INFORMATION FOR SEQ ID NO: 88:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1091 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GTGATTTTTG AAAGATATGG ATGATTGTAG GTATTTATGA TGTCGCACTC AAAATTATTT 60

TCAGGTGCAT ACGCCTTAAA CCCTTTAAAT ATTTGAGTTA AATGATTTAA TACCATATCT 120

AAAGTGAAAA TCATTCAAGT GTTACCTTAT AAGTAATCTC TGATAACATT TTGGCTGTAT 180

CAACAAGTGG AATTGCTGCA GTGTTACTAC CCCTTTTAAA CTTACTTTTG ATTGTATTAG 240

CCTTTAAGGC TGGAGTGACT TGTGCTGATA GTAGATAATT TTCATAGTAC CTTATAAAAG 300

CTTGTCCAAT AGCCTCCATT CCCTATTTAG GGTCAAGATT AAACTTAGAA TTTATATAGC 360

TATTATTGAT ATATTCTCTA AACTCArAAC TACTAGcAAT TTTGGTTAAA TGTTTTCTTG 420

CTGGTAAATT GCTATTCCCT TTTTCATGCA TTTTAGCAAT ACCTGCACGA CCACCAAACC 480

ACCCAATTTC CAATTCCATT TTAAATTCTA GTTTGTCCAT ATAAATTCCT TTAAAACCAA 540

AGTAAAATAT CCGATTGAAG AGTCAATACT AAATATTTCA AAGTAAACTA AATCTGCAAT 600

TGATATTCGG TCTTTTAGTT CATAGTTAAG GTCTTGATAT GTGTAAAGTT TGGAATATCC   660

TTGAATATCA GACATATCAG AATCATAAAG AATTGCAAGT TCTTGTGGCT TTATGTCAAT   720

AATAACTCCT GCGAATTCAG TGTACTTATT TTTATCAAAT ACTCTCTGAT AAGAAGAATC   780

ATTTTCAAGC TTTACAACAG TACCTTTATA AAACTTTAAG GGTTTAGGAT CCTTAAATAC   840

GTTGATCATr CGAAATGACA TATCAGAAAG TCTTTTyCTA ACACCATTCA TTAGACAACy   900

CCCACACAAG ATGGCGTTGA AGTTTCTCTT TTTArTTTTT CTAAAAATGC ATCAAGTTGT   960

GAACAAAAAy TCTTGTTTGA GCCACAACCC CCCTCGCCAC CTTCTTCGCC TCCACTGCTA   1020

CTAGGATAAT AATCAAGTTC AAGTTCATTG AATTTCTCTT TTTTGATCCT ATCAAATTCA   1080

AATTCTCGAA C   1091

(2) INFORMATION FOR SEQ ID NO: 89:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1081 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GGGAAATAAA TTCAAGAAGC AGGTATAATA ATTTTTATAA AAAAGAAGCA GATTTTTTAG   60

GTGCTGCTGT AGAACTTGAG GGGGCTTATA AAGCTATTAA GCAAACTTTA TTATAGATCA   120

CAAGGTATAA ATTTAAGGCT TAAGCCAATT TATCAAAAGA GAGGCATGTT TCTTGGTTTA   180

AAAGCATACT TTGCATACTT CTCTTTTGAG TACTACTATT TGAAAAGCTA TAAACTTTAA   240

CCTAATAGAA AAGCCAAATC TTTTTAAAAA TTTCTAAAAA ATAATTCTAC ATACTCTCCT   300

TATTACATTA AAAAATATTA TTGCTTATAT AAGGCACATA GTATAAAGAC ATTAATCAAA   360

ATTACCTTTT ACTAAGGTTT CAATCTCTCT AAACATGGAT AAGAACTACT TGATCAAGTT   420

ATAACAATCA AAACCCACTT TCTTTAAATA AAAAATCTTT TAATAATAAA ACCAAAATTC   480

CAGCCTTACT AAAGACCCTT ACTCTCTCGT GGATTTAATC TTCTTTATAT ATAAGGGTTA   540

GGCGTATCTA AAGATTTAAT CATTTTGAAT GATAGGGAAG AAGAATTCAT AAAGAATAGG   600

CAAAAGTGGT TTAGTTTACT GGAGCATATA CATTTAATTA TAAATAAGAA ACAATATTTT   660

CCATAAGAAC TGGAGTATAT AAATCATAAG AATAACTATT TTATAAAGAA TAAGTAAAAG   720

TAGTTTAGTT TACTGGAGTA TTTATCTATG TTAAAAGTAA ACGCACGGCG TATAAAGCCC   780

CTACTATAGT ATCCAATATT TTTTGAATTT AGGTCAATGT TGTTTAGTGT GTAAATAAGA   840

ATTATTAAGT GTGAAGATAG CCTATTTTTG CTATTCATAC TTAATATTTC TTTTAAAAAT   900

```
TTTTCCAAAT AGTGCCCCAG TAATTTTTAT TATTTATCAA ATAAAAATAT ATGTCTTTAC        960

ATTTATATTT CTAAATTGCT TAATTTGCAA AGAAATATTT TTTACGATTA AATAGTAGTA       1020

GGATAGTTTA GTTCTAACCG GAGTTTTAGT TTATCTGGTA TTGGTTGATA GTAGnCnTGT       1080

A                                                                       1081
```

(2) INFORMATION FOR SEQ ID NO: 90:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1078 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
GATCCATATG TGTCCCCTTT ATTTTTAAAT AAAAGATATA TATTTAAAGA CAGTTAGGCC         60

TCTTTTAGGC ATATTTTTGT TTAATAAAAA ATATTAAATT AGGGTTTATA ATTTTTATAG        120

ATGAAAATAA AATAGAAGAA TCTAATTTAA CTAAACAATT TTTGTTTAGT TAAAATGATA        180

TAGGGCTTTG CAAAGTAGAT ATAATTAAAG AAAATCTAAA ATCGCTAAAT AAAACTATTT        240

AAACTAAGCC CCATAATGAA AAAGTTTTAG TAAAAATATT AAAGAATATT TTTACTAAAA        300

TAAAAATTAA ACCAGCATTA ATAATACTTA CATTAGATGA TTAGCTACTT TTTTTAATTA        360

ATAAATTTTG CATTTAAAGT TCTATTCCAC TTATAAATAT TGACTATATC AATAATTTTT        420

CaAGCATTGG TACATTTTAT ATTCtAAATA TTTCGTTTTG TCGCTAATTT GTTGACATAG        480

GAATTATAAA AAGGCCATCA TCTTTTAAAT TAAAAGTAA AATAATACTA ATAAATAAAG        540

ACCATCAAGC CCCGTCTTTT TTTTACTAAT AATACAATTG CATTGATTAT GGTTGTTATT        600

GATATTATTT TTTACTTTGA CAATGAATAT GAAAAAATTC TTTATTCTAA ATAAAGAAAT        660

TGGTATTGGT AATTGCAATT TATTATTTTA TTTATATTTT TTAAAAAATA TAAATAAAAT        720

ATAATAAAGA TTTATGGTAG AAAGCAAACA TCAAAAATAT TATTTTTATT CATTATTTTT        780

GTCAGAACTT GCAAGGACTT TGCCACATGC TGTATTAACT ATTATTTTAA TAAATAAAGG        840

GTTATCACTA AAAGATATTG CTATGGTACA AATTTGTTAT ATGGTAGCAA TTATTATTTT        900

TGAATTTCCA TCAGGTGTAA TATCAGATAT TTTTGATAGA AAAATTGTTT ACTTGGTGTC        960

AATTTTTCTA TTAaTGmCTT CTTATTTTAT TGTTGCTAAA ACCTCTTCAT TCGnGTTTAT       1020

TTGTGTTTCA GGTTTATAnA nGGGATGTCA GCnGCnATAG CACTGGCACG ATGACATA        1078
```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1030 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
CCATTTTAAA AAATCAAATT TTACAATACA TTATTATTTG CCACCTTGTA AATATTTCAT      60

AAATAGGGCA TTCAAAATTG GCCCTAGAAT TGCTGCTGTT ATTATCATAA AATGTACTAG     120

TCTGTTACCC ATGCTAAGTT TTTGATTTAA ACTCTTTTCT ACATTGTCTA TTTTGATATT     180

CAAGCCATCC ATTTTTAGGT TTAAATTCTT TTCAACATTG TCTATTTTAG TGTTTAAATT     240

CTTTTCTACA GTATCTATTT TAGAGTCTAA ATTATCCATT TTTAGGTTTA AATTCTTTTC     300

AACATTGTCT ATTTTAGTGT TTAAATTCTT TTCTACAGTA TCTATTTTAG AGTCTAAATT     360

ATCTATTTTT AGATTTAAAT TCTTTTCAAC ATTGTCTATT TTAGTGTTTA AATTCTTyTC     420

TACAGTATCA ATCTTArTrT CTAAATTAGA TATATCCTTT TGTAAATTCT TTTCTACAGT     480

ATCTATCTTA GTATCTAAAC TATCTATTTT TAGATTTAAA TTCTTTTCCA CACTATCTAT     540

TTTGGCATTT AAATTCTTCT CTACACCATC TATTTTGGCA TTTAAATTCT TCTCTACACC     600

ATCTATTTTG GCATTTAAAT TCTTCTCTAC AGTATCAATC TTAACGTCTA AATTGGATAT     660

ATCTTTTTGT AAATtCTTTt CTACGCTATC AATCTTAAAA ATAAGATTAT CAAATTTTAT     720

ATCAAATTGT TTTTCTAAAT TTTCTAAATC TCTATATGTT AGCTCATTGT GATAATATCT     780

TTTAGATAAA TCTTGTGCTA TTAGTTGTTC CATACCCAGT CTAATAAATT CTTTATATAT     840

TTGTTCTTGA GTTACACTTG CAATATTTGT TGACACTGTT TCCATAAAAT TTTCCCTTAT     900

GGTCATATTA TATACTATTT TAGATTAATT GGCTTtAGAG ATTTTTATAT GTAAAATAGA     960

aTTTCTTGCA AGAAAAACCT TTTTGTAATT TACATTTTTA ACTGGGAATA TTTATTATAG    1020

ACTTTTTTCG                                                          1030
```

(2) INFORMATION FOR SEQ ID NO: 92:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1028 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
TTTTGTTGAA TTTCCTGTTA AATTTTCTGA ATTGGTGTGA TTGCTTGTGT TTTTTAGATT      60
```

```
TCTAGAATTG TTGCTTCGTT TTGTTTTTTT TAGACTTTTA GAAGTGGTAG GATTTTTTGG      120

TTCGTTTGGG TTAACATTGC CAAAAGGTGC ACATGATATG CAAATTGAAG TTAATATTGC      180

TGTAATAACG TTAAGTTTAA TAATATTTAA TTTAAAGTTT TTCAAAATAT TCTCCTTATA      240

AATTTGAATT AATATTTATT AATTTTAGTT CAAATATATA ATATTACAAT TTAATATCAA      300

TATCAAATAA GTTTAATATT ATTTGATATT GAAAATTTAA TTTCTATTGA TGTTTTTAGC      360

GTGGATTTAG ATTGCATGAA TTTTAAAAAT AAAAGTTAAT TCTTCTCTTT TTAAAATATG      420

AAGTGTAACA ATTTGTTTGG ATTTAATGGG TTTAATCTAA GGATCAAGAT GAGGAATTTA      480

GAAATTATAA CGAACTAAAA GAACAATTAA AATTAAATTT GAAATCTGAT ATTAATAATA      540

AAATTCAAGA AATGAAAATT CTACACGAAA TTAAGCAAAA ATAACTTTAT AAATATGACT      600

GTTTTAAAAG TTTTAAGCAG TTTATAAAGT CTTATGTAAT TGCCAGAAGT CAAGTGTATA      660

TGTATTTGAA AATTTATGAG AAAGTTTTAG AAGGGTTTAT TTCTATTGAA AAAGTTAAGG      720

AAATGGGGTT TGTAGCTGCA TATAAAAATA TACTAAAGAA CAACTCGTCA TATGTATATA      780

AAGAAACAT GATTGAAGAA AATATAGCAG AAGATGGTGA TAGTCAAAAT ATGTCTATTA      840

AAATTTTAAT TAAAGATAAA GAAGTTTATG ATTTTTGCAA AAAAGATACT AAAAGAATAT      900

CTTTTATTTT AGGGGGGTTC ATTAAAGCAT TATTGAATTA AGTTGGAGAA TTTTTCTTTT      960

TGTATTTTTA TTAGCAATAT ATTTTCCCAT AGAGGCTTTT TGTGTCTACT AGAATAGGTA     1020

ATAAGATT                                                             1028
```

(2) INFORMATION FOR SEQ ID NO: 93:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1002 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
AATTTTTnAA AAAAAAAAAT TTTTTTTTTA AACCCCCAGG GnAAAATTTG GGGAAAACCC       60

CCCCAAGGCC GTCCTTTATG GGTCCTGCCT TTAGCCCCAG AGGACGTTAA AATTGGATTT      120

ATTCAAACTT TTTATAATTA AAAATTGGCAC TGTAAGGAGT TTAAACAACA AACTCAGAGG      180

CTATTGTTAC AATACCCGAA TTTGAAGATT TAGAAATTCA CACAAAAAT ATCTCTAATA      240

TCAGTTTAGA ATTATCAAAA GGTGATAACG TATTGCTACT TCAATCAAGC GTTAATATTT      300

TTGATAAAAA TAACGATAyC CACTTTGACA AACATCATTT TTATATACTT AGTGCAATTA      360
```

1075

GCCCAAAGAC TTTAAATCTA ATTTCTGATA CTGTTAAAAT TAAAGCAAAC AATAAAATTG   420

AAATAGCCAA TGAAATAACT TCCTTAAAAT CAATTCTAGA GAGTATTGTA AGTGCTATTA   480

ATGGAATTAC TGTAAAAGGA CAAGCGGTCG TTGACTATGC AAGCTTACAA ATAGCAACAT   540

CTAGAATTAG CAATAATATT AATAGTTTGT TTAAGTAATT TTTGCTAATT ATGGTATAAT   600

TACTAGTATG GATTTAAGAT TAGGCAATAA TTTTGAATTG GTATTAATA AAGATATATC   660

ACTTGTTGAT GGAATTGATG AACAAAAACA AAGaTTTTTG ATATTTTTAA AAACCTTAAG   720

GGGTAGTTTA AGCTATGCTC CTCATTGGGG ATTGGACTAT TTCTTACTTT TAAAACTGTT   780

AAAAATTAAC AATCTTCACG CTGTAAAAAA TTATTTTCAT GAAATATCTA AAGAGCTTAA   840

CTTAGrTTTA ATAAATATTT CAACTACTAT ACAAGACAAC AAAGCACATA TATCCyTTTT   900

TTTCTCGGGC GATGTTTTAA ATATGGAGtT TAATTTaTGA GCtAGTTTTT GATTCTGrTT   960

TgGcwTTTAA AACGTACAtT AAGGgTATTG TAAGAGCTAA AA   1002

(2) INFORMATION FOR SEQ ID NO: 94:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 998 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGGCATTATG TACTGATAAT GATGATGCTT TAGAAGATCT TTTTAAAAAG AATGCTGAGC   60

TTAAGAGTAT AGAATATTGG GTAAATATTT TAAAAAAATA TTTCAATAAA ACTAATAGAT   120

TTGATGATCT AAATAAGCTT AAAGTATTTA TGTCTGATAA TCGAGACGTT TATAAAACAA   180

AAGTATTAAA ATTCTTTTGC ATGTTGAAAA AAGAAGACA ATTTAATTAT ATATTTGCAG   240

CATAGCAATA TTAAAGCCCC CAAATAGGGG GCTGTTAGCT ATTAGGAACC ACCATTGTTG   300

CAGTTACTAA CCGCATTGTT TGCAAAATTA TCTATATTGC CGCCGCTAAA GAAACCCTGA   360

ACTGTTTGTT TGAAGGTGCT TTTTTGTTGT TCAGAATTAT CCCCAGTACA CTTATCAAGT   420

TCACTCTTTA TATGATTAAG TGCAGATTTT ATTTTGCTTT CATCATATCC TAAAAATTTA   480

TCAAATTCTC CATCATTACC CAGAGCTTCT TTTAACCAGT CAAGGTGTGT TTTCTGGTCT   540

TCAGATAGCT TTTCTCTAAG TAGTTCTTCT TTAGATTTAG GTTTTTCTGG TGTTGCTTCT   600

TTTTGGGTTA AATCACGCTT TCCCCTGCTT TTTGTTTGTT GTGCATTGTT TTTTAAAGTG   660

TCATTATCAT TAGAATTGCA GCTATTTAGT AGTAGTAAAA ATAAACAAAA TAATATGTTG   720

ATGATTTTCA TTGTTATTTC CTTTCCTTAT CTCCAGTACA ATATGTTGAG TAAAAATAAA   780

ATTTATTCTT GTAATTATAG AGCTTATTTT TAAAAATCTT TAAAAATATT AATTGAGAGA   840

TTTATATTTT TCGAATGTTG TGCTAGCnTT TATTTCATTA TTATTGAATA TAGGAGTAAC   900

TAATGAGAAA TAAAAACATA TTTAAATTAT TTTTGCATCA AGGGATTTGT AATGGCTGTA   960

AAGCATATGT AGAAGAAAAG AAAGAAATGA TCATAATG   998

(2) INFORMATION FOR SEQ ID NO: 95:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 996 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAAAATATTT TTATTTATAT TTTATTGTAA TTATTCTTAA ATGATATATA ATATCAATTA   60

AGAATAATTA TTATTTATAA TATATATTCC TACTTAGATA AAAGGAGATA TTTTTATGAG   120

AAAAAGTTTG TTTTTATATA CATTATTAAT GGGAGGATTG ATGTCTTGCA ATTTAGATTC   180

CAAATTATCT AGTAACAAAG AACAAAAAAA TAACAATAAT GTAAAAGAAG TTTCGAATAG   240

TGTTCAAGAA GATGGTCTTA ATGATTTATA TAGTAATCAA GAAAAGCAAA AAAGCTTTAC   300

TAAAAATTTT GGAGAATGGA AATATGAGGA TTTAATTAAT CCTATAGAGC CTATAATACC   360

TTCAGAATCA CCAAAGAATA AGGCTAATAT ACCAAATATT TCAATTGTGC ATACTCAAAA   420

AAAAGAGATA AAAGAGGAGG ATTTAATCCC TTCTACTAAT GAAGAAAAGG AAGCTGATGA   480

AGCAATTAAA TATTTAGAAG AAAATATTCT TCAAAACTCT AAATTTTCTG AATTAATTAG   540

AGAAGTACGT GTACTTAAAG ATGAATATGC TTTAATAAAC TCTGATTTTT ATGATGTAAT   600

TGAAAGATT CACAATAAAA AAACATCATT AATGGAAAAT TATAAGAACA ATAGAGATAA   660

GATAAATAAA TTAACACTGT TGCAAAATAA TTTAAAGATA AATATTGAAC TTGAGCAGCT   720

TATAAATATG ATTGATATTG CAGAAAATGA AATAAGATCT GCGGCTTTCT TTTTTGACAC   780

CGCTCAGAAA AGGTTAAAAG AAAGTATTAT TAAAAGATTA GAGAGTAAAA ATAATAGATC   840

TTATTATGCA TTAGAATTGT CTAGACAGGC TTTAAGTGAC GCAAGAAGTG CTTTAAGCAG   900

TTTAGAATCT TTTGCTTTTA AAAGAGCTGA ACCAATGGTA AGAAAGAAAA AAATAAAAGA   960

GCTTATTAAA CATGCAAAAA CTGTTTTAGA AAGTCG   996

(2) INFORMATION FOR SEQ ID NO: 96:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 986 base pairs

```
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: double
          (D)  TOPOLOGY: linear
```

```
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGACTATAT ATACTAAAAG GGACTTGTGC TTGTATTCTA TTGGCTAGTT GTTCTTTTAC        60

AAGATGAGCG TCAAAGCGTA CATaGTATTG CCAAAAACAG TCATTTTGAG TAAAGAAATC       120

ATATCCTTAT ATAAGGATGT TAGTATTCCC CCGTTTAATG AkATATGTTC ACCAGTCATT       180

ACCGGATTGT AGCTTACATA TTCCGCTTTT CTATCATAAT AATTGATAAC TGGTCTTTTA       240

GAACAACTAG TATTATAAGT GCGTGTTATG AGTTCATTTT TTGGTTTTAT AAAAAACAAT       300

TGAGGAATAT ATCCAAAACC TTTTAGATCC ATTCTAGGAA ATAACACTAA AAAATTATCT       360

GcTCCGAAAA GGGCAAATAT TTGGGTTATt ACATCTCTTA TTATTCGAGT AATCTCCCTG       420

ATTTCTTcTT TtCAATATCA TTAATTTTTT CCTTGATTTT TTTCTTTtCA ATATCATGAT       480

TGTTAGTAAT TTTATTATTA ATATCTATTT TGTTAGCTGC ATTGTTAGCA ATTTTTTTGT       540

TACTTGTCAT AAGTAATTAC CTTTTGTAAA AATTATGGTG TGCTGTTAGC ATTGTCTgAT       600

TTTGAATTTC TTCTTGTAGT TTTTTTAGAG CCGCACCCTC ATCTCCGCCC ATCCATCCAG       660

GTAGCATCGA TTTtAATTTk GCAAAGAAAT AATtAAGATt AAAAATACTT TtAATGCCAT       720

tAATtAtGGG ATAATAAtGT GTGTTTCAAA CGCAAaGTCT TtAAaGTAAT aGTTATCTTA       780

TAAGAGGTCA AGTAAGGGTC CAAGACAGTA GTGGTTAAGT TTTGAAGAGT TTGCTCAGCT       840

GAGGCCAAAT TACTTGAATA CTCTCAGCAT ATTGACTTTT TTGTAAGGCC GAAAGATTAA       900

AATCCTCGAA CATTTCCATC ATCTGGTAAn TCTAGACTCT AGAnCTACTT GTGCCCCGCT       960

TTGCCAGGCC ATTTGGCATC TTCTAT                                           986
```

```
     (2)  INFORMATION FOR SEQ ID NO: 97:

          (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 976 base pairs
               (B)  TYPE: nucleic acid
               (C)  STRANDEDNESS: double
               (D)  TOPOLOGY: linear
```

```
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

ATTGAGCACT CCTTTACATA TTCATCAAGC TCGCTTTTTA AAGAATTAAT TTCTCCATTA        60

ACAACTTGCT TGTTTTTTTT ACTACTTGCT TTATTTAAAG CGTCAATTTC GGCTCTTAAA       120

TTTTCTATTT TAGTATGCAT ACTAACAAGC TCAACACTAG AATATTGCTT AAATGCATTT       180
```

```
ATAAATCCTA ATTCTAAATT AGCCCGCTCT AAATCCAATT CGCTTCTAAC TTTCCTAGCG      240

TTAACTTCTG ATCTAAAGGT TTGCGACAAA AGGTGTTCAA AAGTATCTTC ACTAATTGTT      300

ACTCTAGAAT CCTCGCTAAC AGAAGTTTCT CCACTTTCCC ATTTTTGTCT CATTCTCCAC      360

ACATTTACCC TAGAAACTCC CAATTTAACC GATATTTCTC TATCATCTAA CGATCCTTCT      420

CTAAAGTATG CAACATAATC ATtAAAAGAC CTTTTAGCTC TTTTCAAAAC AATTTCTCCT      480

AAAATAACTA AATTAACAAA TTGTTACTCT AAATAGTAAA TCAATTTGTT AATTGTTAAC      540

ATTAACTATT ATCTTATTGA TATCTATTGA CAGGTGTTTG GTATTTTTTT GACTTTTATT      600

GATTTAGAAA TAGCAATTAA CTAATTTATT GAATTTTGCA ACAACTTGAC TATATAAATT      660

AGGGAAAATC TTTTATTGTT TTAATTAGAT CATCGCTTGT AAAAATTCTC TTATCATAGT      720

TGTGkATCCT TATAAATAGT ATATCTTTAA ATTCGTTGAT CATAATTAAT TGATATTGTT      780

TTGAAACTTT TTGATAAATA TGGTTAAGAA TACCATAAAC AGCCCCCAAA AATATCATGG      840

AATCATACTC TCCTAATTTT TTCAAACATT TCTTTAGCAT CCCTTTCTTG TCGCTATAAT      900

CAACTTGCAT ATTTTTGGAA TTTTTATATT TTTnTATTAA ATATTTATTT TTCAGAACGT      960

CTTTAATAAT TTTnTT                                                      976
```

    (2) INFORMATION FOR SEQ ID NO: 98:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 968 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```
GTCAGGCTTT TTACAGAAAT TATTATAATA AATAAAAGCT TTATTCAATT CTCATGTTAA       60

AGAGCTTAAT AAAGCCGCGG GCTTAGCTCA ATTTATTTTA GATAAACTCA CTAAACGATT      120

AAATTCAGTT CAATTTAGAA TTAAAATTAT TTTGTATTTG TTAAAATAAA AGAACCTATT      180

TAAATTCTCT TGTTAAAAAA TTCAAATAAT TTCTACTTTA AAGCTATATA CTAACTTATT      240

ACTTTATAAA ATTTTAATCA TTCTTAATTT AAAAAATACT TATTGAATAT AGAATAAATA      300

ATTGGAGCAA GTGTTATTCC CATTATTAAA ATTACTTGTA TTGTTCTATT ACTTGCAGTA      360

AGTTCGTTTT TTAAAACATT TATTTTATTA TCTAGGTTAA ATATATCCTT TTGTAAGGTT      420

TTTTCTACAC TATCTATTTT AGTATTCAAG CTAGATATAT CTTTTTGCAA AGTTTTTTCT      480

ACATTATCTA TCTTAGTATC TAAACTATCT ATTTTGGCAT TTAAGCTCTT TTCTACATTG      540
```

```
TCTATTTTGG CGTCTAAACT ATCTATTTTA GAATTAAGTT CATTTTTAAC ACTATCTATT    600

TTAATATTTA AATTCTTCTC TACATTATCT ATCTTAGTAT CTAAACTATC TATTTTGGCA    660

TTTAAGCTCT TTTCTACATT GTCTATTTTG ATATTCAAAC CATCTATTTT TAAATTTAAA    720

TTCTTTTCCA CATTGTCTAT TTTGGCATCT AAATTAGATA TGTCTTTTTG CAAATTCTTC    780

TCTATATCAA TTATTTTCTC TTTTAAAAAT TCAAAGTTGT AATaTCATTA TGCAGAAAAA    840

CAAAATCTAT gCTtCCTgCT AAACCCTATA TTAAAAATTC GTTTTTAATA CCTTTCTAAT    900

GGTTAATAAT GGTTTGGTAA TGGCCTAAAA TTGGTTCCAT AAGGATTAAC CCTTTTAAAT    960

GGTTTATA                                                             968
```

(2) INFORMATION FOR SEQ ID NO: 99:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 954 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```
GCAGGTCGAC TCTAGAGGAT CCCCTTTAAC TAGAATTTTT CAAAATGATA AAACTTTAAC     60

CCGAAATGAT AAAACTTTAA TTTTTGCAAT TTTATTCTCT TGTTTTTTTT AAAACGATTA    120

GAATAATCGT TGAkCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG    180

GTTTTTGCAA GTTTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT    240

TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA    300

AATAAAGAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAATA TTCAATTTTC    360

AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA    420

TATTAATTCT ACTATTAACT ACCCACCTTA TATTCAAACT ATCTTAAAAA TAGAAAAACA    480

AGTTGACGGA AATATTAATG GGATGACTAA AGAAAGTGGC ACAGAAACTA AAAAGCTTTT    540

AGAAATTCTA AATGGGAATA TTTCTCGATT TAAAGATGCA ATTCAATATG GAGGAAGTTT    600

TAGGGCTAAA GATGTTAGAG AAAATCAAAC CCAAAAAGAA AACAACAAAG ACTCGCATAT    660

TCATGTCGAC GATTTTAAAG AATACATACA TTTAATCATG CCTAGCATTA cAATAATGCT    720

GATAGTAGTA GTAGTTATTA CTATACCAAC TACATAATAA ATGGAGACAA TTTGTkAAGA    780

ATTATTAGCA ACTTATAArA AATCTTTATA AATTACCAAT ATTCTTGACA ATTTTAATAC    840

TATTTTTTTT ATATACTATA ATATTATGAA AAAAAATCAA AAAAACAAGT GCTCAGAAAT    900

AGAAAAAACA CAATTAGAAA TAATAAATAA CCAATCAGAA ATAGAAAAAC AACG          954
```

(2) INFORMATION FOR SEQ ID NO: 100:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 946 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```
AGAAGAAAAT AAATTATACA GATCTTCTGT ATCTTTTAGA TATTTTTTTT ATGATGAAAA      60

TACAAAAAAG AAATTAGGGT ATAAAAAAAT AATAACAATT TTCAATTTGC TTGATAAAGG     120

AAGTGATGCA ATAAAGTTTC CCATATTTAA TGGAGGATTA TTTGCACAAG ATAAGGTTAA     180

ATATTTAAAT AATGAAAGTT TACTCAGTAT TAGTGAGATT GAAGAAATAT TAGTCAAAAT     240

ACTTTTCTTT GAAGAAAAAA ATATTAAAGA TAAAAAATTT GTAAAATATT CAAGGCTAGA     300

TCCTAAAAGC TTTGGAGAAT TATACGAAAC TCTACTTGAA TATGACCTAA GAATTGCAGA     360

TACTACTGTT CATCGTATTG TTGAAGACGG GATTTATCTC ATTCGTACTG AAGAAGAGCT     420

TGAAAACAAT AAAGTAAACA AAATTGCTAC ATATCTTAAA GGGAATATTT ATCTTACATC     480

TAGATCACTT GATAGAAAGA AAAGTGGGGC ATATTATACT CCAGATGATT TAACTGATTT     540

TATGGTTATA TCATCAATTG AAGAGCAGCT TAAAACCAAG TCCCCTTTAG ATATAAAAAT     600

CATTGATAAT TCTTGTGGAT CAGGGCATTT TTTAATTTCT TGTCTAGATT ACTTAACAGA     660

AAAGGTATGG TACGAGCTAG ATAAATTTGA AGATGTAAAA AAAGAGCTTG ATAAAGAATA     720

TGGGATTATT CTTAAAGAAA GTGAGGAGTA TGATATTCAA GATAGTATAA GTAAAGAATT     780

GGTGCTTAAA AGGATGCTGC TAAAGAGGTG TATTTATGGT GTTGATATTA ATCCTATTTC     840

GGTTGAAATT ACTATGCTAA GTTTGTGGAT TAATACCTTT ATTTTTGGAA CGCCACTAAG     900

CTTTATTGAG CATCATATAA AAACAGGAAA TGCTCTCTTG GGATAT                    946
```

(2) INFORMATION FOR SEQ ID NO: 101:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 913 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
CTTTGACTCA AAACTTTACC CTTTAAATTG CTAACTTTAA CTTGAAAATA CTAAACTTTA      60
```

ACCCGAAATA ATAAAACTTT AACTAGAATT TTTCAAAATG ATAAAACTTT AATTTTTGCA   120

ATTTTATTCT CTTGTTTTTT TTAAAACGAT TAGAATAATC GTTGAkCAGG TTTATTGATT   180

ATCAATAAAC CTGATCTATA ATATTATAAG CGGTTTTTGC AAGTTTAATA GGAGCTATAA   240

TATCCATGAA CAAATTATTG ATATTCATTA TTTTATTAGT CTTTTCATGT AATTTAAGTA   300

ATTCTGATCA AAATAATCCA CTAAACATGT CAAATAAAGA AAAAATAAGC GAATATCAAA   360

TAAATGAGTC GTCAAACAAA TATTCAATTT TCAAACGAAA TTCAAGCGTT AAAAGATACA   420

CGTTCAACCA TTATTACTAA CCAAAATGAT AATATTAATT CTACTATTAA CTACCCACCT   480

TATATTCAAA CTATCTTAAA AATAGAAAAA CAAGTTGACG GAAATATTAT TATTAATGGG   540

ATGACTAAAG AAAGTGGCAC AGAAACTAAA AAGCTTTTAG AAATTCCAAA TGGGAATATT   600

TCTCGACTTA AAGATGCAAT TCAATATGGA GGAAGTTTTA GGGCTAAAGA TGTTAGAGAA   660

AATCAAACCC AAAAAGAAAA CAACAAAGAC TCGCATATTC ATGTCGACrA TTTTAAAGAA   720

TACATACATT TAATCATGCC TAGCATTAAC AATAATGCTG ATAGTAGTAG TAGTTATTAC   780

TATACCAACT ACATAATAAA TGGAGACAAT TTGTTAAGAA TTATTAGCAA CTTATAAAAr   840

ATCTTTATAA ATTACCAATA TTCTTGArAA TTTTAATACT ATTTkgTTaT ATACTATAAT   900

ATTAAGAGAA AGA   913

(2) INFORMATION FOR SEQ ID NO: 102:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 910 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TCGCTATnnG AGCTCGGTAC CCTGATAAGG CGAGTGTGAC GGGGATTGCT AAGGGAATAA   60

AGGAGATTGT TGAAGCTGCT GGGGGGAGTG AAAAGCTGAA AGTTGCTGCT GCTGAAGGGG   120

AGAATAATGA AAAGGCAGGG AAGTTGTTTG GGAAGGCTGG TGCTGGTAAT GCTGGGGACA   180

GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG TTAGTGCTGT TAGTGGGGAG CAGATATTAA   240

GTGCGATTGT TAAGGCTGCT GGTGAGGCTG CGCAGGATGG AGAGAAGCCT GGGGAGGCTA   300

AAAATCCGAT TGCTGCTGCT ATTGGGAAGG GTAATGAGGA TGGTGCGGAG TTTAAGGATG   360

AGATGAAGAA GGATGATCAG ATTGCTGCTG CTATTGCTTT GAGGGGGATG GCTAAGGATG   420

GAAAGTTTGC TGTGAAGAAT GATGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG   480

GCGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGTA   540

CTGCTGCAAT TGGAGAAGTT GTGGCTGATG ATAATGCTGC GAAGGTTGCT GATAAGGCGA   600

GTGTGAAGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTAAAA   660

AGCTGAAAGT TGCTGCTGCT AAAGAGGGCA ATGAAAAGGC AGGGAAGTTG TTTGGGAAAG   720

TTGATGCTGC TCATGCTGGG GACAGTGAGG CTGCTAGCAA GGCGGCTGGT GCTGTTAGTG   780

CTGTTAGTGG GGAgCAGATA TTAAGTGCGA TTGTTAAGGC TGCTGGTGCG GCTGCTGGTG   840

ATCAGGAGGG AAAGAAGCCT GGGGATGCTA AAAATCCGAT TGCTGCTGCT ATTGGGAAGG   900

GTGATGCGGA   910

        (2) INFORMATION FOR SEQ ID NO: 103:

                (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 888 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AACATGTAAA AGAATAAGCA TTAACTCGCG CATTCTTTGA TTTAAAACAA CCACCCGAAC   60

TACTAAAAAC CTTATTTTCA ATCGAACTCA TTGATTTTGA ATATTTTTTA AATTTTAAAA   120

GAACATCGTC AAGTTCTTTA ACTGAATCTA AATAAGGATC TTTTGCCTGT ACTTCTTCAG   180

CCTGTCTTGT TTGACGTTTA GATCTAGGAG CAACTGGAAT TTCTGATTCT AGCCCTAATT   240

GTGGATTATC ATCAACATTA GGAGCTTTAG CTTGCCCTTT GCCTTTTAAA GCCATAATTT   300

AATTACCTTT TAAAGCTCTA TTCCCAAAAA CACTAGCAAG CACTATAGAT AACTCTTCGG   360

TTAATTTATG TACTTTTGAA AGTGCTATAG CATTAACAGA TTTATCATTT CCCCCATTCT   420

TTTCAAGCTC TCCTTGTGCA TTAAAATGCA GCTTATCACC TGGGTTTACA CCATTTCCAT   480

TTTTCTTAAA TGTTAAATAC CCCGTGAAGT TATTTGTAAT TGGAACTACA GTTGCCATGC   540

CAGTAAACTC ATCTATATCA GTGCATATTC CGTACAAGTC ATCCCCACCA CCAGCCTCAA   600

CTTCTAGTTC TGTTGTACCA TCTGCACTAA AACTAAGCTT GACTCCACGC TTGTATGGAT   660

ACCCTTTAGC AGGATAATTT TCTATTTTGT CTTTACTACT AGTAAAAACT CCATCCGAAT   720

TGGAGTAAAT TAGATTTTTA TCTCTAAAAT CTACAGAATT ACTAAGCAAA CCAGTATCTT   780

GCTGAGGATT TTTCATTAAT GCTTTAATTT CTGCAACTTT TTTATCAAAC TCTTCTTTTA   840

TTTTTGTAAT ACCATCGCTC ATTAAAAACT CCTTTAAGCA ATACTGGT   888

        (2) INFORMATION FOR SEQ ID NO: 104:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 883 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
GATAGTAATT AAGTCCTACA ACCAATAGTG TTACTTTGCA TTAATTTGTT CTTTCCTTAT      60

CGATAGGTCT CTTCCTTCCT GATTGAATTT CAGATCATTA GATATTTTGA GACTTTCTTC     120

ATCAGAATTA ACTCAAGTCA ATGCATTGAT TGATTTTCTC ATTTAATGGA GCTAGTGCTT     180

TATTTATTGC TGGGGTTAAT GCACTCTCAA GTCTTTCCAT ATTTGCTGTA TAGATTAATT     240

TmTAATGAGA ATACAGCTCA TAAACCAAAA AGAATCCTTT ATGTGCAATT TCATCAAATT     300

CATCTTCAAA TTTAGAAAAT ATATCAATAA GGGTTGATAA AGACGTAAGT CCAAGCTCAA     360

CATTATCTTT GGATAATTTC ATAAGTTAAT CTCTTTTTTT AATGTGATTT TTGCCATTAC     420

CATTGCCATT CTTAAAAATC TTGCCTATTA CAATAGTCAA TATGTCTTTT AATAAAGGCT     480

TGAGAAGAAT TAACACTCCT AAAACCAATA CTGTTACAAA AATCATTACG GCTATAAGTT     540

TAATTTCATT TAAATTGATA AGAAGTTCTG TTAATTTAAT AGTATCCATT TTTTAATCCT     600

TTATTTTAAT TTTTTATTTG TATATACATT ATATCAAAAT CGTAATTTTT GCTAAAAAAG     660

TTTGCAGCTT TTAAAGCTGC GGGATGGGGC CCCCTGATAG GTAGGCTCTT TTTTGAATAT     720

ACCATCCTTT ATACATGGGA AATCTACTAG ATAGTCCTTG GGGGAGCGTC TGrTTGCTCA     780

TAAGCCATAC TTGTTTCACT TTCATCGGAA TATCTTAGAT AAAGTACTTT ACTCTCGCTA     840

TTACTGTAGT GTTCTGCGTC AAGCTCAATA TCAAGGTAAA TGG                       883
```

(2) INFORMATION FOR SEQ ID NO: 105:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 857 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
CTATTAATTG CCAAAAAACT AAACCAAACA ACACTTAAAA GGAGAGTCTT ATTGTGATAA      60

TGAGATATAA AATGAAAATT TTAACTAAAA ATAAAACTTA TGAATATCCG CTGAGAGTAC     120

TTCCCGTCTA TGAATGGGAT AAAGTGCTAG GATTTAATCA AAGTGACGCT GTTTTAAAGC     180

TTAATGAGGT TAAATTCTTA AGAGAAATCA CAAGCTTAAT GATAAGTCCA AAATTTTTAG     240
```

ACGAATTCTA TGTGATTTTG GATCAAAATA GAGAATTTAT TTCTTATTAT AAGGACTATC   300

TTGTTGCAAT AATTTACACT GCACAATTTA ATACTTTTCA TTTAGACAAT AATCTAAAAA   360

AGCCCGCTTT AGTATATTTG AGTGAGTATG AAAATAATGT TGGTGATTTT GTTGCTTTtG   420

ACTATATTAA TGAAAATTTT GATTATGAAA AAGTAGCCAC TTCGCTTTCA TCAATTACAT   480

CAAATTCCAA TGAGCTGGTT GCTAAATGAG CAAAAGAAAT AGAGATATTG ATAAAGCTAT   540

TGCAAGTCTT GATGAGACTA GAAAAAAATA TTTTAACTTG CTTGACGAGA TTAAGAACGA   600

TAAATACTTT TTCCCAGTAA TTATGAATAT TTGCTCATAC TACTCGGTTA AAAAATTGCC   660

TTATGACGAG CTTTTAGAAG TCAATAGACT TGCTGAGATT AAATTAGAAA AGAATTGTA   720

TGAATTAATT TTAAGCAAGT GAGGACTTAG TGAGCGACAA ATTCACCATT AAAtTTAAAG   780

GtATTCyTGA TCaTGCTGCA ACAAAAAAGG GCCATTGAAC CAGGATATTT CTAAAATGGn   840

AAAATTATCn TAAACCT   857

(2) INFORMATION FOR SEQ ID NO: 106:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 846 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AGTTGTTCTT TTGCGAGATG CGCGTCAAAA CGTAGCATAG TATTGCCAAA AACAGTCATT   60

TTAAGTAAAG AAAGCATATC CTTATATAAG GATGTTAGTA TTCCACCGTT TAATGATATG   120

TTTTCACCAG TCATTACCGG ATTGTAGCTT ACATATTCCG CTTTTCTATC ATAATAGTTG   180

ATAACTGGTC TTTTAGAACA ATTAGTATTG TAAGTGCGTG TTATGAGTTC ATTTTTTGGT   240

TTTATAAAAA ACAATTGAGG AACATATCCA AAACCTTTTA GATCCATTCT AGGAAATAAC   300

ACTAAAAAAT TATCTGCTCC GAAAAGGGCA AATATTTGGG TTATTACATC TCTTATTATT   360

CGAGTAATTT CCCCGATTTC TTTCTTTTCA ATATCATTAA TTTTTTCCTC GATTTTTTCT   420

TTTCAATATC ATTAATTTTT TCCTCGATTT TTTTCTTTTC AATATCATTA ATTTTTTCCT   480

CGATTTTTTT CTTTTCAATA TCATGATTGT TAGTAATTTT ATTATTAATA TCTATTTTGT   540

TAGCTGCATT GTTAGCAATT TTTTTGTTAC TTGTCATAAG TAATTACCTT TTGTAAAAAT   600

TATGGTGTGC TGTTAGCATT GTCTTGATTT TGAATTTCTT CTTGTAGTTT TTTTAGAGCC   660

GCACCCTCAT CTCCGCCCAT CCATCCAGGT AGCATCGATT TTAATTTTGC AAAGAAATAA   720

TTAAGATTAA AAATACTTTT AATGCCATaA TTATGGGATT AATAAGTGTG TTTCAAACGC   780

AAAGTCTTAA AGTAATAGTT ATCTTATTAA TGAGGTCAGT AAGGGTCCAA GACGTAGTGG   840

TTAAGT   846

(2) INFORMATION FOR SEQ ID NO: 107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 840 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CAATGAAATA GTTAGAGAAA TTAAAAATGT TATTAAAAAG CACAATTTGG AGCTTGATAT   60

TGAGCAATAT CCAATTTCTA TAGAGGGTCA ATATGGCATA GTTGATTATA TTAGGACTAC   120

ATTCTACAGT ACAAGTACTG GATATGAATT TTCTTTTGAT ACGCGAATTC CTACAGAAra   180

TTtACAATGG aACAATGAAA ATGGGTCTAA AGTTACAAAT ACAGTGTATC AGATGTTTGG   240

TTCAGGCATT ACTTATGTCA AAAGGTATGC TTTAGTTGCA GCTCTTGGTA TAGAAAGTGA   300

AATAGATACT GATGCAGCTC CTATTTACAA TAACCACGAA AACGAAAATT CTATGCCTAG   360

CAAGCAAGTT AGTGTTAATC AAAAGCAAGA ACAAAAAGA GAACAAAAAC AAGAAAAAAA   420

TCAACTAAAC AACTTTAATA AAAACTTAAA ATCTGGCAAG GCTTATTGCT ATGAAATTTT   480

TAGAGACGCA CTGTTTAATA TAAAAAATTG GGTAAATGAA GGTGAAGAAA AAAATAATAT   540

AAATGCTCTT ATTCGGGCAT TATGTACTGA TAATGATGAT GCTTTAGAGG ATCTTTTTGA   600

AAAGAATGCT GAGCTTAAGA ATATAGAATA TTGGGTAAAT ATTCTAAAAA AATATTTCAA   660

TAAAACCnAT AGATTTGATG ATCTAAATAA GCTnAAAGTT TTTATGTCTG ATAATCGGGA   720

TGTTTATAAA ACAAAAAnTA TTAAAATTCT TTTGCATGTT AAAAAAAAAA AAGACAATTT   780

AATTATATnT TTGCCAGTGT TGCCATATTA AAGCCCCCCA ATAAGGGGGC TGTTTAnATT   840

(2) INFORMATION FOR SEQ ID NO: 108:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 814 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGACTTT GTTTTATCTA CAATAACTTA TTTTAGTTTG AAAATTACAA GCAAGCCTGA   60

AACCATTCAT TATCCCTATG GACACAAACT AATGGAAAGC TTAATAGCTT TTATCATGGG   120

AATAATTATA CTTATGACAG GATTTACACT ATTTCTAAAT ACAACCGGAT TAAATAAATT   180

TATCACTCTT GGGGGAGAGT CTGGATTTAA TCTACACATA CACCAGAACA AAAATAAAAA   240

TGATACTATA TATGAACATG ACCATTGCCA TTCACACGAT CACGATCACG ATCATAACCA   300

CGACCACAAC GAAGAAGACA AAAAAAACAT ACTAGAAATA TTTCAAATA AATGTCTAGA   360

AGCAAAAGCA AGCTTTCGAT AAAACCCGAA GTTGTTTCGC TAAAGTGACA AGGATTAAAC   420

AGGATTGTAT TTTTCAGCAG CCTATTTTAT AAACGATCTG CATTTAGTAA ATAGTTTTTA   480

GTTAGGAAAT AATGTAGGAT TACTAAGTGT GATGTCTGAG AGAAGGGACA AGTATTGTAG   540

CGAGCTTAAA TCCTTATTAT CGTTGGCCAG TAATTTAGAG GTAGGGGATC GGGATAAAGG   600

ATTGGCCAGT TTATAAGTTG GAGGGAAGGG CAAAGGATGC CTTAAAATCG GTAATCGCTC   660

CTTAAGGTTT AGGGTTAACA AGTTTGGCCA CCAATTAACC TCCAAAAAAA GGCCAGGCAA   720

AAATACCCAT TAAAGGCAGG ATTTCCGGTT TGGGAATTGG CCCCGGACCA CCTCCAAAAG   780

GGCCATGGAA GGTTTGGGAA ATTGGTTAGG TAAA   814

(2) INFORMATION FOR SEQ ID NO: 109:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 808 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCAAAACCA GTTCTATTTT GTTCAAAATC AATATTCGAC TCTTCAGAAT TTAGTTTTAA   60

ACTTTTGATT TCATATTTGT TTTCAAACTC TTCAGTTGAT TCAAATGCTA TTATCTTAGC   120

TATAGGTACT TCTTGACCGA ATATTTTATA GTTATTGTCA TTAATGCTAT AATTAAGTAT   180

AGCTAAAGGT AAGCAATGAA TAAGTTTTGA ATCGGATGGG TGAAAAAATA TAAGAATACT   240

TAAGCTCTCT AAGATTTTCA ATTAAATTGT TATTTTTATC TTTTATATCT TTTAAATCAC   300

CAGATTTTGC CCATGTAACA TAACCACTTG CAAGTATTTC AAATGCCTCT CCTTCTTTTA   360

TTTCGTTTAA TTCGGGTTCC TTAAAGGTAA GACAAATATT GCTATTACTC TCTTCAATGG   420

GCTTTTTATC ATATTTTATA ATATTTCCCT CTTCAATTAT CTTAAAATCC AAAACCTCGG   480

TTTTGATACT GTTGATTTTT GAAGATTTTG GTGTAGTCAA AAAGCATGAA TAAAATAATG   540

GTATATATAA AAATATATTC AAAATACATA TGTTCTTTTT CATAAAATTT TTCCATTAAT   600

TGTATTTCTT TCTATTTCTC TCTTCACTTT TAAATATTGT TGATAAGCAG TGGGTCTAGG   660

CATAAAACGA TCATACTCAG GGCTCCCCTC TTCGCCAGAA TACTTAATAT CTGGAGAATA   720

TAACTCGCTT ATACATGAAT ACAGCCAATA AACTTCACTT TTAAATTTAT TATTCTGCTC   780

ATTTTTTACC CTACCAAACA ACTTAATC   808

(2) INFORMATION FOR SEQ ID NO: 110:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 804 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TGGGAAACAT TATATCTAAC AACCCCTAGT GGTACTTTAC TTGAGGGGGA CATAGAAATT   60

GATGGCCTCA ATTCAACTGG ACAACGAAAA TCCTACAAAA TATCGCTAGG AAAAAGAAAA   120

TATGTTTATA TGAAAGTAAA GTATAAACTT GACCTTAAAA ACTATCTCTA CTTAAACATA   180

GACTCTCAAA TTAGAGACAT TTATTCTAGG ATTATTTCAA ATAACTATTC TGATATGGGA   240

ATTAGCTTTG AATATCAAGA CTTTTTTGCT CCAGTTAATG AAGTTAAAGG AATTAAATTT   300

ATGGAAATAA GTGCCTGTAT TAAAGACACA GACACTGAGA GTATTGCAAA AATTACTGAT   360

AGCGATTTTA AAAAAAATCA AGATATTACT ATTACTGATG ATACAATGCT CCTTTTCAAT   420

ACTACAGATA GATTGCTTAT TGATATTGAT AGTTAACAAA TATGAAAATA CCTAATTTAT   480

TCAATGGCAC TGAAGTTCAT AAATTTATAC TTACAGAAAC AGAATATGCA CAAGCATTGC   540

TTAATGAACT CAAGTCTCTT AATTCTAACT TCCTATCCAT TAATGTAATA GAAAATATAA   600

AATCAAGATA TATTGCAATA TGGATATCTC AAGTTTATC TATCTTTTAT GCAAAAACTC   660

AAACTTTACA AAGTATTACA AGCAATATTA ATAGCGTTAT TTTTGCTTTA CGCCATATTG   720

GTACTGATGA GTCGTTTAGA CTAATTTTCA aGGCCTTTTa AATGTGGACA TGAAGTTACT   780

ACTCCTGAAG CGGGGGTATG GAAA   804

(2) INFORMATION FOR SEQ ID NO: 111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 800 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```
GCGTGAGATG TTAATTTTTA CCnGCTTTAA AGCAGAATAG TCCATCCCCA TGAGGAGCAT      60

AGCTTAAACT nCCCCTTAAG GTTTTTAAAA ATATCAAAAA CCTTnGTTTT TGTTCATCAA     120

TTCCATCAAC AGTGATAAAC GTTATTAAAT ACCAATTCAA AATTATTGCC TAATCTTAAA     180

yCCATACTAG TAATTATACC ATATTTAGCA AAAATTACTT AAACAAACTA TTAATATCAG     240

AATTAATTTG AGCGGTTGCT ATTTTTAAGC TTGATTCGTC AATTACTGAG TCCCCTATAA     300

TTTTTATACC ATTGATAGCA CTAACAATAT TATCTAGAAT TTTTTTTAAG CTAGTTGTTT     360

GGTTTGCTAT TTCAATTTTA TTATTCGCTC TAATTTTAAC AGTATCAGAG ATTAGATTTA     420

AAGTCTTTGG GCTAATTGCA CTAAGTATAT AAAAATGATG TTTGTCAAAG TGAATATCGT     480

TATTTTTATC AAAAATATTA ATGCTTGATT GAAGTAGTAA AACGCAATCA CCTTTTGATA     540

GTTCTAAACT GATATTAGAG ATATTTTTTG TGTGAATTTC TAAATCTTCA AATTCGGGTA     600

TTGTAACAAT AGCTTCTTGA GTTTGATGTT TAAACTCCTT TACAGTGCCA ATTTTAATTA     660

TAAAAATGTT TGAATAAATC CAATTTTTAA GGTCTTCTTG AGCCAATGCC TGGCCATAAA     720

GGCGTTGATT CATTCtGTAA ATTTCATAGT CTTCaTTCaT TCtAATTCyA GTCCCCTTTA     780

tTTTTTACgt TTTGTATTAG                                                800
```

(2) INFORMATION FOR SEQ ID NO: 112:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 798 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```
GAAATAGCTT TTTAAGTTTT CTAAATCATC TTTAATATCA ATAACTTCTA TAAAGTATTA      60

ATGATGAATT TTTGGGAATG TTTTATGGAT TTAAAAGATT AACAAGACCA CTTTTTTTAA     120

ATACGAAGAT ATTATTACAA AAACTATCAA AACTGTACCC ATGTATAAAA TTCATTACAT     180

AGAATTTAGA TTTAAGAAAG GAAGTGTTTT TTGTTATATA AAAGCAATTC ATGTTTTAAT     240

AAAAAAAGAA AAATTTAAAA AAAATATGCT CAAAGTCTAT TAGAGAGAAT AATTAATCTA     300

GAACATAAAG TATTAAAGAT AAAGCAATTT TTTTAAAAAA TATATAAAAA TCGAAACAAA     360

AAATTAAAGA TATAGTAAAA TTGTATTTGT AGCAATATAC TTGTGCTAGA GGCTATGAAT     420

CTCTAAAGAT TTTAGCAGGG GAGAAAATAT GAAAAAAGT TTTTTATCAA TATACATGTT     480

AATTTCAATA AGTTTATTAT CATGTGATGT TAGTAGATTA AATCAGAGAA ATATTAATGA     540
```

GCTTAAAATT TTTGTTGAAA AGGCCAAGTA TTATTCTATA AAATTAGACG CTATTTATAA   600

CGAATGTACA GGAGCATATA ATGATATTAT GACTTATTCG GAAGGTACAT TTTCTGATCA   660

AAGTAAGGTT AATCAAGCTA TATCTATATT TAAAAAAGAC AATAAAATTG TTAATAAGTT   720

TAAGGAGCTT GAAAAGATTA TAGAAGAATA CAAACCTATG TTTTTAAGTA AATTAATTGA   780

TGATTTTGCG GGATCCGT   798

(2) INFORMATION FOR SEQ ID NO: 113:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 798 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AGCTTTTGCA TAATAATTTT CATCAAATAA TTCCCATATT AAATCCTCCC AAATATCATT   60

AATTTTTACT TACAGCTTTA TTTCCAAATA CTGCTACTTT TATTAAATAA ACATCGTTAC   120

TAATTTGTTT TGCATCAGAC AACGCTATTG CATTAATAGT TGCCTTATTT GGTGGTGCTC   180

CAGTCACCTT TTCAAGAGCA CCGTCTTTAT TAAAAACAAG TTTGTCTTTT ACTTTAAGCG   240

TAGAATCTTT TGCTACTAAA TAACCCTCAA AATTATTTGT AATCGGAACA ATAGTGGCTG   300

TTTTGCTAAA CTCATCTATA TCAATGCATA TTCCGTATAA ATCATCTTCA CCACCAGCCT   360

CAACGTGGGG TTCATAGTGA ATTTGATCAG CTTTTTCCTC TTGAATAACT CTTTTTACCC   420

CACGCTTATA TGGATACCCA GAAAATGGAT GATTTTCTAA TTTGTCAAAT TTGCTGGTTC   480

TAGTGCCTCC AGAGGCAAAA AATTGTATGT TTTTATCTCT AAACTCTACA GAATTGCTAA   540

GCAAACCAGC GTCATGCTGG GGATTTTTCA TAAACTTTTC AAGTTTACTT CTCTTCTCTT   600

GaTAATCTTT TACTAATTGC GTTGTGTCTG cCATTTGTTT AACTCCTTTT ATTGcCCAAG   660

GgCkAwCCrC CAGCTtCAGG TGTTACTGTT TTCTCAAGGG CCTCTATTGG CCAAAAATTG   720

GCAAACTTTT TTTTTAAATT CCCAAAAAAA AATTTTTAAA AATTTAAAGG GAAAAATTTA   780

AACCCTTTCC CCTTTTTG   798

(2) INFORMATION FOR SEQ ID NO: 114:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 783 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
GGACTCAAAA CTTTACCCTT TAAATTACTA AATTTAACTT GAAAATACTA AACTTTAACC      60

CAAAATAATA AAACTTTAAC TTGAATTTTT CAAAATTACA AAACTTTAAC CCAAAATGAT     120

AAAACTTTAA TTTTTTGTAA TTTTTACATA AAAGTGTTAA CTTTAAAATC CCAAACTTTA     180

TAATTTTGGG AAATTATCAA TACTTTTTTA ATTTATTCTT TATTTTCAAA ATAATCTTTA     240

TATACTTATA TATTATGTAT AAGGCTATAA AAGAACAACA AGAAATAGAA ATAGATCATG     300

CATGCAGAAT ACTTATTCTT ACCGCAACAA TATTTGAAAT AAATTCAATA TTCGAAAATT     360

ATTATCAAAA AACTCTACTC AAAAAGTATA ACGAAAATCT CAAAAACAAA AATCTACCTC     420

CTAGTAATAT ATCAACAATG AAAAAATACT TAAATCAATT AGAAAAGAA ATAAAAATCA     480

TAGCAAAATT CTATTTTAAA AACGATCAAT CTCTAATTTA TTGCAAACTT AATTATACCC     540

TAGAAAAAAT TTGTTTAAAA CTAATAAAAT TCTACAAAAA ATTCTACAAA GAATTAAAAC     600

AATTTACACA AAAGAACATT ACTACTTAAT TGTAAATACA TTATAAAATA ATCTTATGCA     660

AATATTTAGA AATACAAATT GTAAAGATAT ATATTTTTAT TTAAATAAAT AATAAAAATT     720

GCTGGCACAC TAATTTGGAA AAATCTTTAA AAGAnATACT AGGTATGAAT AGCnAAAATA     780

AGC                                                                   783
```

(2) INFORMATION FOR SEQ ID NO: 115:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 768 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
TTCTATATAA ATATTTTGTA ACTTTTTTGC TTATTACAGA CTAAGCCTAA ACGTCCTACA      60

ACCCCATAAA TGCAACGCTC TGCAGCTTGA CACATTTAAA GTTTGGGCTA CTCCCTTTTC     120

GCTCGCCACT ACTAAGGGAA TCTCTTTGAT TTCTTTTCCT CAGGGTACTT AGATGGTTCA     180

CTTCCCCTGG TATCGCCTCT ATTATTTAAA TAATAGATAG CTAGCATCTT GCTAGCTGGA     240

TTACTCCATT CGGTAATCTT GGGATCAATA AATGTTTGCT TCTCCCCCAA GCTTTTCGCA     300

GCTTACCACG ACCTTCTTCG CCTTAAAGCT CCTAGGCATT CACCATAGAC TCTTATTACT     360

TTGACCATAT TTTTATCTTC CATCTCTATT TTGCCAATTT ATTTATACAA CATAAAATAA     420

TATATATCTT TGTTTAATAC ATGTCAATAT ATATTTTATT TTTTATGTTA TTTAAACAAC     480
```

ACATTCAAAA ACACCAATAT TTAAAAAACA TAAAAATAAA ATCAAAGTTT AAAGTATAAA   540

AATAAAAACC CTGGCAATAA CCTACTCTCC CGCGAACTCG CAGTACCATC AGCGAATAAG   600

AGCTTAACTT CTGTGTTCGG AATGATAACA GGTGTTTCCT CTTTTCTTTA ACCACCAGGG   660

TTTTTACAAG GAAGACAAAA ATATgGcCAA AGATACGGGT AATTAGTATT AGTCAGCTTA   720

ATATATTGCT ATACTTACAC TTCTAACCTA TCGACCTGGT ATTCTTTC   768

(2) INFORMATION FOR SEQ ID NO: 116:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 765 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CTTTACGCCT AACTTACCCT CCACGTGTAC AACCCCTTAA CAACCCCTTA ACTTACCAGT   60

GACCCCCTTA ATATGGTAGT TATGGGGGAA CGCTTAGAAT AAAAAAGTCA TCTACGACAC   120

CCCCGATCAT AGACCTGACT CTTGTTATCC CAAATCACTT CAGCGCCCTC GCAACTTATG   180

GGAAAAAGTT CCTAGAAAGA TGTATAGAGA AGTGGAATCA AAGTAATAGG CAATTCGCAA   240

GTGAATAAGG GAGAAAGGAT TTCCTATGTT ATAGGGAGAC GCTAGACATA GTGCTTGCGA   300

GACTGGATTG TGCTTGATGG ATAGAACCTA GTTTAGTGTG TACATCCAAA AAATGGACTA   360

AATCAATAGT ATAAGGCGAA TTGCCAGCGA TGAGGTCTGA ACCAAATTGC CTCACATCAG   420

GCGATAACAG TTACTACTAA CAGTTGCCAC TTCGGCTACT CTATCTTGCG TGCTTATTGT   480

AGCACTCTGG AGGTCCTGTT GTTAAGCCAG CATTAGCACA GCTCCTCCAC TGCGGGTTGC   540

GAGTATAGAG TAGTCCTAAC TGGCAAGGAT TCCCCCTCTG GTTGCTAGAG GTCGAATTAC   600

CCACCCAACA ATAGTTGCAT TGTTGGGGGG GTGGGTACCT ACTACTCGGC ATATACTCCC   660

CCCCTTTCGA GACCTCCCTC GAGGGTCGAG GGAGCATTTG ATCATAGACG TTCATCCCAG   720

ACATGGCCTT TCGGGTTTGA CGTCTCGCGA CCCCCCTTCG GGGAC   765

(2) INFORMATION FOR SEQ ID NO: 117:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 755 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GAGCCATTAT TGGCTCCTAT TTTACTAGCT GCACTTGAAA TTCTTTTCTT TTTTAGGAAC   60

AAATAACGCT CTTTAAATTA AAAGGCATAA TGCTATATTG TATTCTAAAT CATATACAAA   120

GGACAGTTCT TTATATCATA AGTGCAAAAA TAAAGTCATA AATTCAATAA AAAGGAGGAA   180

AACTCTTCTA GAGTAGTAGA AGAGCAACCA AAAATTAATG AAAATTTTTC TACACAAGAA   240

TCTATACAAA AACTGCCCCT TTACTGCAAC ATACAAACG TGAATCTTGT ATATTACAAT   300

AATAGATAAT ATTATTGCAA CAATCCTAAA TTACAAATAC AGAATATGTT ATTAGCCCCA   360

AAAAGGGGCT AATACATTTA CTTTAAATTA CAAGTTATTC GAACCATAAT TGTTCAATAT   420

TAATTTCAAA TCTTTTCTTA TAGCAAGAAA TTTTTCATAA ATCAATATTA GATAATCATC   480

AAAATTGCTT TTATCAAGCA CATACAAAAG TTTAAAAAAA TCTACATCAT CAAGACATAA   540

ATAGAATATG AAAACCTTAT TTTCAAACAC ATTATCACCC AGCTTTACTT TAATTTTACG   600

AAAAAGGTTG ATTAATTCTT TAGACTTTTT TGGCCCCAAA TTAAAAAAAA ATTCATTTAA   660

AATGTTTTGA CTTTTAGGCG GAGACAATAT ATTTATTGTC TCCGCATCAT TTTCTATATC   720

TAAGAATCGA CTCATAGGAA CTTATAAATG ACTTT   755

(2) INFORMATION FOR SEQ ID NO: 118:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 753 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CTCAGCCAAG ATACTGGTTT GCTTAGTAAT TCTGTAGATT TTAGAGATnA AAATCTAATT   60

TACTCCAATT CGGATGGAGT TTTTACTAGT AGTAAAGACA AAATAGAAAA TTATCCTGCT   120

AAAGGGTATC CATACAAGCG TGGAGTCAAG CTTAGTTTTA GTGCAGATGG TACAACAGAA   180

CTAGAAGTTG AGGCTGGTGG TGGGGATGAC TTGTACGGAA TATGCACTGA TATAGaTGAG   240

TTTACTGGCA TGGCAACTGT AGTTCCAATT ACAAATAACT TCACGGGGTA TTTAACATTT   300

AAGAAAAATG GAAATGGTGT AAACCCAGGT GATAAGCTGC ATTTTAATGC ACAAGGAGAG   360

CTTGAAAAGA ATGGGGGAAA TGATAAATCT GTTAATGCTA TAGCACTTTC AAAAGTACAT   420

AAATTAACCG AAGAGTTATC TATAGTGCTT GCTAGTGTTT TTGGGAATAG AGCTTTAAAA   480

GGTAATTAAA TTATGGCTTT AAAAGGCAAA GGGCAAGCTA AGCTCCTAA TGTTGATGAT   540

AATCCACAAT TAGGGCTAGA ATCAGAAATT CCAGTTGCTC CTAGATCTAA ACGTCAAACA   600

AGACAGGCTG AAGAAGTACA GGCAAAAGAT CCTTATTTAG ATTCAGTTAA AGAACTTGAC   660

GATGTTCTTT TAAAATTTAA AAAATATTCA AAATCAATGA GTTCGATTGA AAATAAGGTT   720

TTTAGTAGTT CGGGTGGTTG TTTTAAATCA AAG   753

(2) INFORMATION FOR SEQ ID NO: 119:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 747 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TGATTTTAGC TGTTTTGTAA mCCAAAAGTG GATTATAATA ATTGGGCCTA CTAGTCTGAA   60

TCCTAGAGTC AATAAAACTT ACACTAATTG TATCTTGCGG CAATTTCGTA TTCCTCCTTT   120

AAAATTTCGA TTGCTTTTAC ACTAGCATTG AATGCTATAG ATGCACTGTA TGCATGGTTG   180

CTATATTTTG TGCCTAAATT AATCAGTCCA ACTGTTTGCA TATTAGATGT TGGGTAAATG   240

TAGAAGTTAA TTTTATTAAT ATATTCGGGT TGTAGACTGG GCAAAGTATA CTTATGAGCT   300

TTATTGTGTA GAAAGTCACT AAGCATACTA TAAAGCATTA ACATGCGTGA ATTAGCrTCA   360

AAGTCTTTGG CGTTTAACAC TATTGCAATA ATATATATTT GAAAATTTAT ACTAAATTCC   420

AAAGCATTyT CATAAAATAC ACCkGCTyTA kAATTATGAT CAAATAGATT TTCTGTACCA   480

GCAAATTTCA ATGCTATTAT ATTTGAGCTA GCAGCTGTGA TTTTTGAAAG ATATGGATGA   540

TTGTAGGTAT TTATGATATC GCACTCAAAA TTATTTTCAG TTGCATACGC CTTAAACCCT   600

TTAAATATTT TAGTTAAATG ATTTAATACC ATATCTAAAG TGAAAATCAT TCAAGTGTTA   660

CCTTATAAGT AATCTCTGAT AACATTTTGG CTGTATCAAC AAGTGGaATT GCTGCAGTGT   720

TACTACCCCT TTTAAACTTA CTTTTGA   747

(2) INFORMATION FOR SEQ ID NO: 120:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 744 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACACTTAATT CAAAAGTACT AAGCTTTAAC CCGGAAATCT TAAGAAGATT TGAGAATTGT   60

AAATTTTAAC CTAAAAAGCA GAACCTCATA AAAGTTTGAC TTTTACCCAT AACAGTATAT   120

AATATTAATA TGTTTTTTTT CAAATTTTTT TCAAAACATA AACCTGCTAG GAAAAAAAAT   180

TATCATAAAA TCAATCCGGA TGAATTCATT CTAATTAGCG AACATCTTAT CAATTCTTAC   240

AGCATTACTC ACCAATTACT TGGGATTATC ATGGCCTCTG GAATTCCATT AACTCATATA   300

AAAAAATCAA AACATCAAAA CTCCTTACAA TTTCAAATCT GATATATTTT CTTATACGTT   360

GAACAACGGT TTGCAAATTC AAACACATTC TCTAATTTGC TCTAACAAAA TTTCTAGGTG   420

TATTGAAAGT TTAAACAAAA ACAGATTACT ATCTATTGGT GCAGACAAAA TTAATTATGT   480

AGCAAAAAAT ATTTTTGATT TTAGAATTAC TACTAAACAA CTAAAAATTA TTCATTCTTT   540

GATTGCTAGG TCAAAAGAAA CACTACATGA AATCAGATAT AACTCTCATT CACAAAACTT   600

CTTTTTAGTT AAAACACCCT GTATTTTAAA TCTGTACCAA AAGCTCAAAT ATATCAAGTC   660

ATTCGGCACC TCTAAAGCTC AATCAAAATA ATCTAAATTA TTATCGAAAC AGCTCCAATG   720

AGCTTACATC TACTATTACA AATT   744

(2) INFORMATION FOR SEQ ID NO: 121:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 721 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

AGTTTGTnTA TTCCTAGTAA CAATAACATT TCAGAATAAA GTTTTGTnAC CAAAAGTTtT   60

CTTCAGCcTC AACTTGTGTT TGTAAGTTTT TTTGTTCGCT CACCTCGATT TACCTTATGT   120

TTTTAACTTT GTTTAATATG TACTTGCAAA ATAGTTTTTC TAGTAGCAAG TAACCCTCCT   180

AAAACAAAAT CAATGTATGA ATGAGCAATA TCAGTTGAAT CTTTATCCAC TTGTTCATTT   240

GGTGTAGGTA ACATATACTT GCTAGGTTTA AACTTAATAA GCTCTGGGTT TAATGGGTAA   300

ATAAGTATTT GATGTTTTAG CAAGTTTGAA GTTTCAATGT AGACATCTTC TCTATTATTA   360

ATAGCCyTGA TAGTTTGAAT CAAAACATCC TCCCATTTTT CGCAGCTACT TGCTGCACCC   420

TGTGCTGCTG CGTATGGCTT TACGAGTTTG AGCGAaGTTG TAGGgTCAAC TATTACCATC   480

ATAGGTGTAG AAAATtCGTC TCCTAGCTCT AACTTtGAAA GTCCCGCCTC AATTTTTtCA   540

AATATTTTAT CCATTTTATC TTTATCACCA CTAGCAACTT CTTCTTTTAC TTGATGTGGC   600

ATATTAAGAA GTCCATACAT ATTGGGAAGT AGACGTTTTT GATTTTTTCC ATCTTTTTGA   660

ATTGAAACAG TGCCTGTTAG TACAAAGTGA TTAATAAGTT TAATAATCTC GCTACTTGCA   720

A   721

(2) INFORMATION FOR SEQ ID NO: 122:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 720 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
CAATTTCAGC TCTTAAATTT TCTATTTTAG TTCGCATACC AGTAAGTTCA ACACTAGAAT      60

ATTGCTTAAA TGCACGTATA AATCCTAATT TTAAATTAGC ACACTCTATA TCTAATTCAC     120

TTATAACTTT CCTAGCGTTA ACTTCTGATC TAAAGGTTTG CGATAAAAGG TGTTCTAAAG     180

TATCTTCACT AATTGTTACT CTAGCGTCCT GGTTAACAAT ACTTTCTCCA CTTTCCCACT     240

TTTGTCTCAT TCTCCACACA TTTACTTTAG AAACTCCTAA TTTTTTCGCT ATTTCTCTAT     300

CATTTAACGA TCCTTCTCTA AAATACACAA CATAATCATC AAAAGGCCTT TTAACTTTTT     360

TCAAAACAAT TTCTCCTAAA ATAACAAAAT TAACAAATTG TTACTCTAAG TAGTAAAGCA     420

ATTTATTAAT TGTTAACATT AACTGATAAC TTCTTGATAT TTAGCGGGGA ATATTTGTTG     480

GCCTTTATTG ATTTAGTTCG CTGCTATTTC TATAATTTTT GATTTAGAAA TAGTAGTTCA     540

TTAATTTATT GCATATTACT ATAAAATAAT TCTACTTTTT CGGAAAAATC TTTCATTTCA     600

TTCATAAGAT TTTTACTTGT GAAAAGTCTT TTATCATAAT AGTGTATACT CAAAAATAAA     660

ATATCTCTAA ATTCTTCAAT CGCATCtATT TGAAAGTCTA ATyCTAATAC TTTTCTCCTA     720
```

(2) INFORMATION FOR SEQ ID NO: 123:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 715 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
TAATAAAAAA CTAAAGCTGT TCAACTGCAA TTGTTGCACT TGAAATTTTT TATACTAAAA      60

TAAAATACAA ATAATTATAT TAACAAATAT CGATTTTTAT AAAAAATAAG TAAAAGTAGT     120

CTAGTTTACC TGAGTATTTA AATACTTTTA ATTGAGGATG TTTTATTTTA AAAAGGAGTG     180

TAAAACTATG TCAAAAGCTG TTGACGAAGT ATATTGCTAT TCTTGTGGCA AGATTTAAAA     240

AAGATGCTGA GATTTGTATT TCTTGCGGAG TCAGAAATAA ACAAACCGAA AACTACAATA     300
```

```
AACTTATAGT ATTTTTACTA TGCTTACTTT TTGGTTATTT AGGAGTTCAC AGATTTTATG        360

TAGGTAAAAT AGGAACTGGT CTATTATACC TATTTACATT TGGATTTTTA TATGTTGGAG        420

TTTTAATCGA TCTTATTAGA ATAACAACAA ACAAGTTTAA ATGTAATTAA AAGGATTCTT        480

TAGTAAATTT TTTATTAGTC TTGTTAAAAT TATTTTTTAA TTTTTTAAGC ACATTTTGTG        540

TGAACTGCTA TTTCTATAAT CTTTGATTTA GAAATAGCAG TTCACTAGAT AATAATAAAG        600

CTAAAATTAA TATyTtAGTA TTTAATAATT CTTGAgAAAA nGTAAAATTG GTATATGTTT        660

ACTTGTTATA AAAAAATCTA TCTGGGTAGG ACTTTTAATG TTTAATAAAA TAGTG           715
```

(2) INFORMATION FOR SEQ ID NO: 124:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 715 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```
GGAGGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC         60

ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT        120

GTTGATCTAC AAATGGGATA TCAAAAAACC GTAAAATGGG ACGCGTTTTT AAATGCTAAT        180

CCTACAACAA TTGCCAATGA GGTTAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG        240

GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG        300

AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT TCCTTTTGCT        360

CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAAACTTA TTAATCACTT TGTATTAACC        420

GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAT        480

GGGCTGCTTA ATATGCCCGA GCAGATAAAA GAAGAGGTTG CTAGTGGTGA TAAAGATAAA        540

ATGGATAAAA TCTTTGAAAA GATTGAGGCT GGACTTTCAA AGTTAGAACT GGGCGACGAA        600

TTTTCCACCC CGATGGATGG TAATAGTTGA CCCAGCAACG TCACTTAAAC TAGTAAAACC        660

ATACGCnGCA GCACAGGGTG CAGCAAGTAG TTGTGAAAAA GGGAAGATGT TTTAA           715
```

(2) INFORMATION FOR SEQ ID NO: 125:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 714 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```
GTATAAAAAG CAAAAGAAAA ACATCTTCCT TCACAGAATA GTTGCCCAAA TCCAATAATA       60

ATTCATACTG GTTGAAAAAT TTCCAAGAAA ACGCAAATTA TTATTGGTGT TCATATTGTT      120

CAACATCTAG ACCAAACCGA AGTGGAGTGG CCTTTTTCTT ACTTCATTTA GTAAGTTTTC      180

AATAATTAAA CCAACAGGTA GTATTAAAAC AAAGTTTTAA TACTACCAAA GTTTTAATGG      240

CTCCTTCAAA ACAGCAGTTT TAACCGTTTC ATTCTCTCTT CTGCTAATAG TAACTGGTCA      300

TATTTAGTCA TTCCTCTCAA AACACCAATT GATGTAGCAA CAATTATCAA ATTACTAACA      360

TTAAAAAACT AAAAATATTA TAAAATATCC AAAAATAAAA ATATTCTTAT TAATTAAATA      420

ATTAATACTA ATTATTTAAT TATAGTATTA TTGCATTATA TTATAGTTAA GGAGAATATC      480

TATGAAATAC CATATAATCG TAAGTATATT TGTTTTTCTA TTTTTAAATG CTTGCAATCC      540

AGATTCTAAT ACCAATCAAA ATAATTCTAA AAAGGAATTA AAAACAGGAA GAATCCCTAA      600

TAAACAAATA AAAAATGCCC TACTTGgATG ATTTAAAAAA TTTAATAGAA ACAGCTAGTG      660

CAGGATAAAA AAATATGAAA AAAATTAGGA AGAAGAACCT TCAAACCAAT ATGG           714
```

(2) INFORMATION FOR SEQ ID NO: 126:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 708 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
GnATTAACTG GGAAAAATTT CTCAAGTGTA ATTTTATATT CTTTTATATA ATTTTCATTT       60

AAATCGAAAG TATCGTTCTA TGCTATCCCC TTGTTCAAGT CTTCACGTTC ATGAATGGGG      120

CCTAAAAAAT TATCATCACC GCCTATTAAT TCCAATAAGT GTTTTCATTA CCAAAATTAC      180

ATTTTTTGCA TATTTTTTAG TTTAAGTTTA TTAATTCTTT TTTTACTTTC GTTTTCTCTT      240

TTTTATTTTT TATTTTTATA AATCACTTTT ATTTAAAATA TATGTATACA TATATTTTTT      300

TTACTATCTC TTTTAATAAG CCCAGACAAA TAATTACAAA TATCACACAT TAAGCAACAC      360

ACGTGCTCTT GCAATTTTGA TTTTTTAAGC CAATCTCCAA AAAATTTTTA AAAAACTTAT      420

TATATTTATT GATTGCCCyT TAAGAAACTT TTTTTATTAT GCyTTTATTA TAACTTTGTA      480

AAyCTTtCAA TAGTTTAACT TAGATAGATC GGAAAATACC TTGnCTATTA GGGCTTTATT      540

ATAACTGTTA AATTTTGnCn TTTTTTGTTA AAATTTATAT TGCCAATGAT AAAAATACGC      600
```

CAATTTAAAT TAAACATTTT AATAATGTCC AAATCCTCCT TATATAAGGC ACATCATAAA   660

TCAATTTTAC TGAAAAAACA AAAAGCATAT CTAAGATTTC ACCCTATT   708

(2) INFORMATION FOR SEQ ID NO: 127:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 703 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGCCAACATG AACTATAGCC TAAAAATCTA AAAGACTAAC TTGAATTTTC TAAAAATCGT   60

AAATTTTAAC TCAAAAATCT AAACCTGCAA AATTTTAGAT TTATTACAAA GAAGTCTATC   120

ATAAACTTCG TATAATCTTG TTTCAACTCT ATCTAATCTG GCTTTAAATT CATTACCAAA   180

GCAACTAAAT CTTTAGTTTC AAATTCAAAT ACCACTCTTT TATCTAAATT ATCTATTTTA   240

AAAACCTTTA GCAATATCTC AGTTCTTTTT TTCTACCTCA TTTTTTAGTT TAAAATTTTA   300

TTTTTTATTT TTTTTATTAA CTTATTTATG ATAAAAAATT TTATTATTTA GTAAATAATT   360

ATCATATCCT TTTATTAAAG AAGAAATATA ATCTTCTCCT TTTTTTTTAT TCTTTAATGC   420

CTTAAAATCA CCAAGCAAGG TGATAAAATC TTCCTTAGCT AATGAGTAAA GACTAGCTAT   480

AATAAAATTA TTTTCATTTT CTTTTTCTTT AAAAAATTCA TCTTCTTTAT CTAGTTTCAG   540

TATTTTATTA ACTTTTTCTT TATCAAACTT AAAATATTCT AAGTAAAGTA AATATTTAAA   600

GTTTTCGGGA TCATTTTTGG CTATCAGTAA AGAAGTATTT TTTGCAAGAT TTAAATATAA   660

AGGATTACTT AAAATTTCCT TTTCTTCGGG TTGAGGCATT GGG   703

(2) INFORMATION FOR SEQ ID NO: 128:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 699 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCGACTCAAA ACTTTACCCT TTAAATTGCT AACTTTAACT TGAAAATACT AAACTTTAAC   60

CCGAAATGAT AAAACTTTAA TTTTTGCAAT TTTATTCTCT TGTTTTTTTT AAAACGATTA   120

GAATAATCGT TGAkCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG   180

GTTTTTGCAA GTTTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT   240

TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA   300

AATAAAGAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAATA TTCAATTTTC   360

AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA   420

TATTAATTCT ACTATTAACT ACCCACCTTA TATTCAAACT ATCTTAAAAA TAGAAAAACA   480

AGTTGACGGA AATATTATTA TTAATGGGAT GACTAAAGAA AGTGGCACAG AAACTAAAAA   540

GCTTTTAGAA ATTCCAAATG GGAATATTTC TCGACTTAAA GATGCAATTC AATATGGAGG   600

AAGTTTTAGG GCTAAAGATG TTAGAGAAAA TCAAACCCAA AAAGAAAACA ACAAAGACTC   660

GCATATTCAT GTCGaCAtTT TAAAGATACA TACTTTAAT   699

(2) INFORMATION FOR SEQ ID NO: 129:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 695 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GTGGCAAATA ATAATGTATT GTAAAATTTG ATTTTTTAAA ATGGTACATT ATAATATTGA   60

TAAAGAGTAT TATCAATTAA CACTTAATTT TTGCTTTTTC ATAAATTAGA ACTTATTTGA   120

ATTTTTTAAC AAGAGAATTT AAATAGGTTC TTTTATTTTA ACAAATACAA ATTGATTTTA   180

ATTCTAAATT AGAATATATT CAATTATTGA AAAGCTTATT TAAATTATTT TAATAAGCAA   240

ATTTGATTAA ACCCTAACTT TATTAAAATA ATTTATGTAA AAAGTTGTCA AAAATAGTTT   300

TTGTTATACA TATATATATG TATGTAAATA GCTAAAAAAG TTTATTGCTA TCAAAACAAT   360

CCAATCAAGT TGGGTTTAGC TAAGTTCTTA GATAAGAGAA TTTAAATAAA CCCAACTATT   420

TTTTTGTAAA ATTTTTTGTA AAAAAGCCTG ACAAAAATAG TTTTTGCTAT ATACTTATAT   480

TTTTTACTAT AAAAGGAGTA AAAAGATGGA AAATCTTTCA AACAATAATA ATCCACAAGA   540

AAATATTCAA GGAGAGCTCA AAATGATAAG TATTAATCAA CAAAGTTTTA CTGGTTGTGA   600

AATATTTGAG GAAAAATCTT CTCCCATTAA AGAAAAAGT AAATTAAGTA AGATAGGTAA   660

GAAATTACCA GGAATAAGTA GTCAAGAATG TTTTA   695

(2) INFORMATION FOR SEQ ID NO: 130:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 684 base pairs
       (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CAAGCAAGGG TTAACAACTA CCTTAAAGAC AAATTTAATA AAAAAGGGAA TCTAAATTTA   60

GAGGAGTGTA ATAATAATAA TAATAATAAA GAAGAAGAAG AAGAAGACAT AAGAAATAAT   120

AAAATAGAAA AATGTCAAAT AAAAAAATAT TTCAACAAAT GTAACTTTTT ATCCGAAGAA   180

GCTAAGTCCA TTTTAGAATT AAACATTAGT AAGAATAAAA CAATTGAAAT AATAAAAATA   240

ATAAAAAAAA TTGAAACCGA CTTAACAAAA AATAAAAACA AAGTTTGTTT TAAGAAAAAG   300

CAAAAAATGT TGAAAGAAAT ACTAAGCAAA ACTAAAAAGC AATTAGAAAA AAAAGGATAT   360

GACACCAAAC AACTGAAACT CAAAATCGAA AACATATATA AAAGTTATAA AACCAAGCCC   420

CATTTTATTA TTGAAAATAA AAAATACAAA GACCTAGACA AAATAAGGCT TAAACTAGAA   480

AAATCAATTG AAATTAAAAA AGAAAGTATT ACAAAAAAAT ATATACATAT AAAAGTAAAT   540

ATTTTCAACA TACTAATAGA ACAATTGAAA AAAGrmTTGG rAATAAAAAC TTTAAAGCCA   600

ATTATAAAAA ATTATCTAAA TAGCnAAAAA ACCCTAGAAT ATGATAAAGT GTTCAATACC   660

TATTATTATG nACTATTAGA AACT   684

(2) INFORMATION FOR SEQ ID NO: 131:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 673 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GTATAAATTA TCTTTTAAAT TTATTACTAA ATCTCAAATT AGATATATAC TTTGTGTTTG   60

TGCATAAACC AACTCCAGCT TTAAACAGAT CACAAGCGCT AAAGAACTTA CTAATCTACT   120

TGCAACAAAC ACCAAAACTT TGAAATAAGA AATTCAGTCA ACCTTAATAG CAAATCAAGA   180

AAAACCAAAT CTAGATATTG ATAATTGACG TACAAAAAGA AATAGACAAC ATAATTTCAA   240

ATCTAAAAGA GTTTATTAAA ACTCTACAAA CCCTACATTA AAATCTGCTT AGCATAGCTA   300

AGTATGCTCA ACAACATCTT AAAAAATTCA ATTCCAAAAA TAAAATCTAA AAATTGCACT   360

ATTATTTAAA TATCAAAACT TAATTATTAG GAGGTAATAT TAATATGAAA AAAATTTTCA   420

CATTAATATT AATTTTTAGT TTAACGATGC AAATCTTTGC TTTAAATTTC ACTTCAAAAT   480

1101

ATAAAATTCA GAAATATGCT GAAAGAGAAA AGGAGTTCAT TCAAAACCAG AAATTAGAAA   540

AAATTTTGAA AGACCCCGAA AAGACTAAAA AGGCTCTTTT GCAATACGAA AAAGAACAAT   600

TGATAGATCT ATGGATTCCA GTAATGTTAA ATTTATTTTT ACCTTTTGGA GTGGGGcTTT   660

TGTCCAGGAG ATT   673

(2) INFORMATION FOR SEQ ID NO: 132:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 660 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CGAGTATTTT GACTCAAAAC TTTACCCTTT AAATTGCTAA CTTTAACTTG AAAATACTAA   60

ACTTTAACCC GAAATAATAA AACTTTAACT AGAATTTTTC AAAATGATAA AACTTTAACC   120

CGAAATGATA AAACTTTAAT TTTTGCAATT TTATTCTCTT GTTTTTTTTA AAACGATTAG   180

AATAATCGTT GAkCAGGTTT ATTGATTATC AATAAACCTG ATCTATAATA TTATAAGCGG   240

TTTTTGCAAG TTTAATAGGA GCTATAATAT CCATGAACAA ATTATTGATA TTCATTATTT   300

TATTAGTCTT TTCATGTAAT TTAAGTAATT CTGATCAAAA TAATCCACTA AACATGTCAA   360

ATAAAGAAAA AATAAGCGAA TATCAAATAA ATGAGTCGTC AAACAAATAT TCAATTTTCA   420

AACGAAATTC AAGCGTTAAA AGATACACGT TCAACCATTA TTACTAACCA AAATGATAAT   480

ATTAATTCTA CTATTAACTA CCCACCTTAT ATTCAAACTA TCTTAAAAAT AGAAAAACAA   540

GTTGACGGAA ATATTAATGG GATGACTAAA GAAAGTGGCA CAGAAACTAA AAAGCTTTTA   600

GAAATTCTAA ATGGGrATAT TTCTCGATTT AAAGATGaAT TCAATATGGA GGTAGTTTTA   660

(2) INFORMATION FOR SEQ ID NO: 133:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 656 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

AGCACTTTAA AGAAAAAAAA GAAGAAAGAT ACCAAAATAG AGTTGCCAAC TATTTCAACA   60

AAAATTCTGA TTCAAAAATG GGTAGTGTGC AATTGGGGGA GTGTAATAAT AATAATAATA   120

ATATAAAGA AGAAAGAAAA ATTAACGAAA TAGAAAAGTA TCAAGTAATA AAATACTTCA   180

ACAAGTGTGA CTTTTCATGT AAAGAAATTC TTCCAGTTTT ATTAACATTA AATATTGATA   240

AAGAAAACAT AATTAAAATA ATAAAAATCC TAAAAATAAC CGAAATTAAC TCAAAAAATA   300

AAAATATACG CCCTACTAAA TCTTGTATTA AAAAAAAACA AGAAAAATTA AAGGGAATTC   360

TATGTAACAC TCAAAAAGAA TTAGAAGAAA ACGGGTACAA TCCCAAACAA TTAGAAATAA   420

ATTTTCAAAA AATATACGAA AATTACAAAT ATAAACCCCA TTTTATTATT GAAAATCATA   480

AATATAGCGA TTTAAACAAC ATAAAACGTA AATTGGAAAA GTCAtTGAAA GAAAAAAAGA   540

AATTCTCAAC AAGATTATGA aATTTAAAGA TAAACGTTTT CAATATCCTA TTGAACAACT   600

AAAAAAAGAA ACAATATTGA nTTCTAAAGC CCTTATAAAA GAATTTTGAA TACCAn   656

(2) INFORMATION FOR SEQ ID NO: 134:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 652 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

TGnAATTAAT GTATCAAGCG ACTCTTTGTA TCCAGTACTT TTACTGTAAA ATGTAGTCCT   60

AACAACAGGA ACTTCACCAT TTTTACCATA CACAAAAGTT GGAAATTGCC AAAAACCAAG   120

CTTTAAATTG TGATTTTTTA TAACATTTTG AATTACTTCT ACTATGACAT TGAAATCTTG   180

ATACTTATAT CCGTATCCTT TAAGACTTTT GTCAATACGT GGCAAGTTCA TTCTTAAAGT   240

ATCCATATCA TTTAAAAAGT CTATTTCTGC TTGAATATTA TTTTGTATTT CTTGATTATT   300

ATTGTTTGAA ACATTGTTCA TGTTTTCCTC CTTTATTTAG TAATAAATAA GTATATAGCA   360

AAAACTATTT TTGTCAGGCT TTTtACAAAA ATTTTTACAA AAAAGAAGTG GGACTtAACC   420

AAACTCTTTT CTTAAAGAAT CTCGTTAAGT CCCCACTATA TTATTATTTT TTGCAAATTA   480

CTAAATAAAG GTAGTCAAAC TGAAATATGT TCAAATAACT ACGCTGTTTG TAGTGTAGCC   540

CAATTTTTAA TTAAAATCAA TCAATCTTTT ACTAAGTTAT AAAAAGTATA TTAATTTAAC   600

AAAATTAATA ATTAAAATTT AATATTTTTT TAGAAAAGTA TTTAnCTTTA AA   652

(2) INFORMATION FOR SEQ ID NO: 135:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 649 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

nAATTCGAGC TCGCGTACCC AGAAAGTTCA GTTAACAAAA TGTAGTCATG ACTACCTAGT   60

GTCACTTCAA TGTTGAAAAC ATAAGTTATT GTTTTGGGAT CTCTTAAGCT TATTACAGGC   120

ATACCTTTAT CTTCACTACT AATCACTGCT CTTGTTGTAG GTTCGCTTGT AAGCTCTAGC   180

TTGCCACTAT GTAACTGCGT ACCACCAATT GAAAAATAAA CTTCTCTTAA ATCATAAAAT   240

TGCATTTTTA GACCCCCTTT TAAGCACTTA AGCTGTTTTG ATAATCAAcT ATATCTTGAG   300

TAGTAATTAC TAAAGCAACA GCATTAATGC TAAAGTTATA AGTAATAkTC ACGCyAAGTT   360

CTAATTTAAG TTGyGGkGTA GGAGAAAGAG TAAGAyTTAA ATTTTTrTAC TCwATwATCA   420

GTCCTCTATC CACAAACCTT TTCAGTAAAC ATTCAATTGC TGAAGTATAT GCATTGTCTC   480

TAGCTCCACT AAGCTGCAGT GCAGATAATT TGCTATTTTG CCTATTGTTT TTGTTCCAAA   540

TTyTAATAAG CTCAATAATC GCTTCGTTTT TTATATAGTG GTATGTAAAT TGTTCGTCTA   600

TTGyACyTCC AGCTAGGTCA ACACCTTCTT TAAAGGCAGG TAAACCATC   649

(2) INFORMATION FOR SEQ ID NO: 136:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 644 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

TAAGCAAAAG GnCCTAATGT TCAnGATAAT CCACAATTAG GGTTAGAATC AGAAATTCCA   60

GTTGCTCCTA GATCTAAACG TCAAGCAAGA CAGGCTGAAG AAGCACAAGC AAAAGATCCT   120

TATTTAGATT CAGTTAAAGA ACTTGACGAT GTTCTTTTAA AATTTAAAAA ATATTCAAAA   180

TCAATGAGTT CGATTGAAAA TAAGGTTTTT AGTAGTTCGG GtGGTTGTTT TAAATCAAAG   240

AATGmGCGAG TTAATGCTTA TTCTTTTACA TrTTCAAGCT TTGCAGACAA AATAGAAGAA   300

TACCTTTATG ATCCAGCAAA TAGTTTTCCA TATAAGCGTG GGGTTAAACT TGTTCCAAAA   360

GAGAAyTCTA TATATGTTGA AGTTGGTGCT GATACTGATA TGTATGGGAT ATGTGTAGAT   420

GTATGTGAGT TTAGTAGTAC TGCGTATGTA TTACCAATTA CGAATAACTT TGAAGGGTwT   480

CTTGTTACAA GAAATCCGAG TATAAAAATG GGaGAAATAT kGGaTATAAA TAACAATGGG   540

GTTATaTCAA GGCTGGTGGT GGGCCmCCAA cCGyAATTAa TGCATATGCC CTCTCTGaTT   600

CATTACAATC AATTTTGGCA CCCGAAGATG AAGATCAAGA TCAG   644

(2) INFORMATION FOR SEQ ID NO: 137:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 636 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

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AAAAAGTAAT GAATCATGCA TGCAGATTAC TTATTCTTAC CATAACAATA TTTGAAATCA        60

ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA ATTTTATAAC GAAAATCTCA       120

AAAACCGAAA TCTAACTCCT AGTGTTATAT CAACAATAGA AAAATACTTA AACCAATTAG       180

AAAAAGAAAT AAACGTCATA GTCGAATTCT ATTTTAAAGA CAATCAATCC ATAATTTATT       240

ATAAACTTAA TTACACCCTA GAAAAAGTTT GCTTAAAACT ACAAGAATAC TACAAATTAT       300

TCTACAAAAA ATTAAAACAA TTTTTACAAA AAAACACTAC TACTACTTAA TTGTAAAAAA       360

TTATATCTTT GCAAATTAAG CAAATTTAGA AATATAAATT GCAAGATAT ATATTTTTAT        420

ATGATAAATA ATAAAAATTA CTAGGAATAC TAACTTGGAA AAACTTTTGA AAAAAATAAT       480

AAAAATGAAT TACAAAAATA AGCTATCTTC TCACTTAATA ATTCTTATTT ACACACTAGG       540

CGACACTGAA CTAAATTTAA ATATTGAGTA CTATAGTAGG GGCTTTATAC ACCACGTGTT       600

TAATTCTAAC ATACATAAAT ATTGCAATAC TACTGA                                 636
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(2) INFORMATION FOR SEQ ID NO: 138:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 632 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

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CCAATAACAT GACTTTAAAG GTTGCTTATT GACAATATGT TATTTTTCAA CTTTGTTGCT        60

TGAGAACTTT TTTTTTCAAT TTGCTTGTAA AGTTCCGTTA AATGAGATTC AAGCTTAGCA       120

ATATCTGTTT TTATAGAATC CTTATCATCT TGATAATCTA ATAAAAGTTG GTTTAACATG       180

TCTGATACGA TTGATTTCAT GGATAATAAT TTTTCAAACG AATTTTTAAG CTTCTCTAAA       240

TTTGAAATTT CTAGTTTATC TAAAGCATCC TTTTTAGGAT ATAAGTGATT AATCGCTGTA       300

TCAAAAGTTC TTCCAAGGTT GCAAAAAGTG CCAAATAGGA GGGTTTTTTG TTTTGATTGA       360
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ATTAAAATCT TTGAAAGATT CGCTAACTTA TTGGTATTAA TAGGATTTAA AGTAGCATAA   420

GTGAATTTTC TATAGTTTTT AGATCTATCG GTATTATCTG CTACCGTTTC ATATGATGCT   480

ACCCAATAAA TTTCTTTGAA AATTGATATT CCATATTGGT TTGAAGGTTC TTCTTCTAAT   540

TTTTTTTCAT ATTTTTTTCT ATCCTCGTTA GCTGTTTCTA TTAAATTTTT TAAATCATCA   600

AGTAGCTTAT TTTTTATTTG TTTATTAGGG AT   632

(2) INFORMATION FOR SEQ ID NO: 139:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 628 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

GACTTCTTTA ATAGATCAAA AAGCTCACTT CCATCACCCC CAAGAACACT ATTAACAGCG   60

GGGATCCTCT AGAGTCGACC TGCAGGCATG CAAGCTTGGC ACTGGCCGTC GTTTTACAAC   120

GTCGTGACTG GGAAAACCCT GGCGTTACCC AACTTAtCGC CTTGCAGCAC ATCCCCCTTT   180

CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAn   240

CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA   300

CACCGCATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGCCC   360

CGACACCCGC CAACACCCGC TGACGCGCCC TGACGGGCTT GTCTGCTCCC GGCATCCGCT   420

TACAGACAAG CTGTGACCGT CTCCGGGAGC TGCATGTGTC AGAGGTTTTC ACCGTCATCA   480

CCGAAACGCG CGAGACGAAA GGGGCCTCGT GgATACGCCT AwTTTTATAG GkTAATGTCA   540

TGaTAAtAAT GGtTTCTTAg AACGTcAGGg GGCAyTTTTC GGGGGAAAAG TGCGGGGGAA   600

CCCTAATTGG TTAATTTTTC CAAAATAC   628

(2) INFORMATION FOR SEQ ID NO: 140:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 621 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

ATACCGCTAA ACTCATCTAT ATCGGAACAC ACTCCATATA AATCGTCTCC ACCACCAGCC   60

TCAACTTCTA GTTCGGTTGT TCCATCTCCA AAACTAAGCT TAACACCCCG TTTATACGGA   120

TACCCTTTAG CnGGtAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC CCACCAGAAT   180

TGGAAAAAAT TAGATTTtGG TCTCTAAAAT CAATAGAATT GCTAAGCAAT CCTGAGTCTT   240

GTTGGGGATT TTTCATTAAT GCTTGAATTT CTGCAACTTT CTTATCAAAT TCTTGTTTAA   300

TTTTTGTTAT ATCACTCATT TAAAAACTCC TTTAGGCAAT ACTTGTTCTT TTATGTCTTT   360

TTAGATTTTC ATAAAATTGA ATTCGTCTTT GCTTGTATGT ATTACTTATC GCTTGTACAA   420

ATTCTGTGAA ATTAATAGGT ACAAAATTAG AATCAAGCAA ACTTGCTCTT TCTTCTGATT   480

TAATAGCAAT ATTCCCCTTA ATAGAGTCAA CAGAAGAAGA ACTGCTACTC GCATTTTTTC   540

TTAATTTAAT ATTCACTTTT GCTAAAGAAA CAAGTTGCTC TAATATCTCT CCATCGATAT   600

GACTTATGTC TGATACTTTG G   621

(2) INFORMATION FOR SEQ ID NO: 141:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 608 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCCAACTAAT AGTTATTGAT TTGTTCTTGT AGTCAGACGA TAAGCGTTGG TCCGTATGCA   60

AAATTtCTTC CATGTGAAAA ATCTGATGGT GCTCCAAGCA GTTGTTTTGG AACGGGTGTT   120

TTTTGAATAC TTGAAGAAGA CATTATCAAA AGATCATCAT TTCTAGATAG AGTGGCTGAT   180

GATATGCTAT TTGTAAGGCG TGATTTAATT TTACTAAAAA GGTTAGAAAT ATTAGTAGAA   240

TCGTTGTTAA TTAATTTGTC CGTTATTTTA GCATAAATTG TTTCTACAAA ATCTGTATTG   300

GCTGCAAGTT CTTCGGCAAT TGTAGACTTA ATTATCTGCT TAAAATAGTC TAATCCTTCT   360

CCTTTAAATA TTTTGTCTTT AGAAGCATCT AAAAAGTTTT TAAAGGTGAT AGCATTACTG   420

CTTGCAGCTC CATCATCAAG CAGTAAAAGA TCAGTATTGT TAACGGTCGT AACCTTATTT   480

AAATCTTTTA TTTGAACCGT TTCTTCTTCA TCAATTAGTA ATTTTTCTTG ATCATCAGCC   540

ATAAAACCTC CTTAGTTGTT AAAAGTTATA ATATTGTTAC CATCTGTATT ATTAATTTTG   600

AGAACTCT   608

(2) INFORMATION FOR SEQ ID NO: 142:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 591 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CTCCAATAGC GCTAAAAGAA TTAAATATAC TTGCTACTGA TGCTAGTTTA TTTATATCTT   60

GAATAATATT TGCGAATTCC TTTAATTCAT GAGGATCCAG GGGGCTTAAA ACAGTATAAG   120

TGTGTCTTCT ATATCTTATA GATCTTTCGG TATTGTCAGA TATATCTTCA GTCCCTGGCC   180

CCCAATTCAA TCCCCTAAAA GACGTCATCC CGTAATGGTC TTCAGGTTCT TTTTCCATAC   240

TTTTTACATA TTTTTCTTTA AAATTGTAGG CCGATTCTAT TTGCTTTTTT AAATCATTAG   300

ATAGCGTATT TTTTAGTTGT TGTTTTCTTA GTTCTTCCTT CTCTTCTTCT TGTTGTTTTT   360

TCTTAAGCTC TTCTTCTTGT TGTTTTTTCT TAAGCTCTTC TTCTTGTTGT TTTTTCTTAA   420

GCTCTTCTTC TTGTTGTTTT TTCTTAAGCT CTTCTTCTTG TTGTTTTTTC TTAAGCTCTT   480

CTTCTTGTTG TTTTTTCTTA AGCTCTTCTT CTTGTTGTTT TTTCTTAAGC TCTTCTTCTT   540

GTTGTTTTTT CTTAAGCTCT TCTTCTTGTT GTTTTTTCTT AAGCTCTTCT T   591

(2) INFORMATION FOR SEQ ID NO: 143:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 586 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTGTTAGTGT CCCCATGTGA ATGGGTGCAC TAAAAAATTA AAAAAATAAA TTTAATATAG   60

GAGGATTAAT TAATGCTTAT TAATAAAATA AAACAAGATA ATAGAACTTT AAGACCGGAG   120

ATACAAAAAT GGGGTTGTTa CTTTTTGTGT CTGCATTATT ATACAAGTCT ATTTAAGCAA   180

CGTGAATTTA ATGCATATGA AATAAATACA GCGTATTATA GATTTATAGG ACTTGGTTAT   240

ATCAAGAGCA ATTGTTTTAT TATAAATCCA TGTATGATAC TTAATTATTA CGGAATTAGA   300

AGTAGCGTGA GATATGAAAC TGCAAATTAT TTGGGTGCAG CAAATGAATT TGAAATAAGT   360

GAAGTTAAAA TCGATAAGGk TAATGGATAT CACTTTATAT CAACAAAAAA TAAAGAAATA   420

TTATATGATT CACTTGaTTT AAAGCCACGT GGAAAAATAT TTAAAGTAAC TTCmAAACGT   480

wTwTTTAAAC tGrAATAGTT TaCTAAgTTT AAGGCACTTT TaGCACATTC ATAgCTgAAT   540

TTaTTAGCAG rAGrTAGGcC GTAGGATATA ACCAATTTCA TTGGTT   586

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 585 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

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GTGTTTTTTA GCAATTTATT TTCAACTCTT TTTATGTTTT TGATTATTTT AATCATAGTA      60

TCTTTATCAA CATTTAATGT TAATAAAAAT GGAAGAATTT CTTTACATAA GAAGTTACTT     120

TTGTTGAAGT ACTTTATTAC TTGATATTTT TCTATTTCGT TAATCTTTCT TTCTTCTTTT     180

ATATTATTTT TATTACTTAA ACACTCCACT GAATTTACAC TACTATTTTT GGAAACATTG     240

TCTTTAAAAT GkTTATTAAC TCTAGATTTA AATCTAGAGT TTTTTyGyTC TTTAAAGTAC     300

TTGTTGATTT TCTGGTAACA yTCTTTTTTA GGATACTTTA GCTTATAGTA AATTTCAGTT     360

CCACAATTTA CACCCATrTG TTGGTAGTAA TTAGTTGTrA CTTTTAATAC TTTTTCTAAT     420

TtGTAAAGAT AATTTtGCAT tGTTCTtAGw GTAGTGGGAG CTAGACCAkT CcTTTTtAGA     480

TTTtCryTAw AGyArTAGAG TATGTTTTGT TGCGTGTATT TCTTATCTTT TTTGGTTAGG     540

TAATCTAGCG TTGAAGTAAG AGAGATTAAT TTGTGTTGGT GTTTG                     585
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(2) INFORMATION FOR SEQ ID NO: 145:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 575 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

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GGGAGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC      60

ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT     120

GTTGATCTAC AAATGGGATA TCAAAAAACC GTAAATGGG ACGCGTTTTT AAATGCTAAT      180

CCTACAACAA TTGCCAATGA GGTTAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG     240

GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG     300

AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT tCCTTTkGCT     360

CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAAACTTA TTAATCACTT TGTATTAACC     420

GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAG     480
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GGCTGCTTAA TAGCCCGAGC AGATAAAAGA AGAGGTTGCT AGTGGTGATA AAGATAAAnG   540

GGTAAAATCT TGAAAAGATG AGGCGGACTT CAAGT   575

(2) INFORMATION FOR SEQ ID NO: 146:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 571 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

TTGGTTCCCA nCnTATTTCG TTGAAATTGT GATACTTATA GCCATAACCT TTAAGATTTT   60

TATCAATCCC CGGCAAGTTC ATCCTTAGGG TTTTCATATC TCTTAAAAAG TCAATTTCTG   120

CTTGATTAAT TTCTTGTGGA TTATTGTTTT TGCGGTTTTT CATTTTTTTA CTCCGTAAGT   180

TATAATTTTC TTATATATAA ATATATAGCA AAAACTATTT TTGTCAACTT TTTTTAATAA   240

AAATTTTTGT TAAAAGACTT AGGGCTTTGC TAAATTCTCT TTTAAAAGAA CTTAGTAAAG   300

CCCTAATATT TTTACGATCC AATATTCAAG TAGGAAATAA TGAAAAATTA TTTCCTACAA   360

AACTATATTT AGTTTAGTTC AACCTTAAAT TAAAATCAAT TAATATTATT ACACTGCGGT   420

CTATAAAAAT ACAAAAATAT AAAGCTTTTA TAAAATCTTA TTTTAAAAGA ACTTATAAAA   480

ACCTATTCTC TAAATTATTT ACAAAATTCT AAAATTAGAT TTTTAGTTCT TCATATTTCC   540

TTAAAAGTTT TTTAAGAAAA TCTTTTTGAT T   571

(2) INFORMATION FOR SEQ ID NO: 147:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 555 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AAGCGTATAA GCTTGCAAGT AGTGAAATTA TTAAACTTAT TAATCACTTT GTATTAACCG   60

GGACTGTTTC GATTCAAAAA GATGGGAAAA ATCAAAAACG CCTGCTTCCA AATATGTATG   120

GGCTGCTTAA TATGCCCGAG CAGATAAAAG AAGAGGTTGC TAGTGGTGAT AAAGATAAAA   180

TGGATAAAAT CTTTGAAAAG ATTGAGGCTG GACTTTCAAA GTTAGAACTG GGCGACGAAT   240

TTTCCACCCC GATGATGGTA ATAGTTGACC CAGCAACGTC ACTTAAACTA GTAAAACCAT   300

ACGCAGCAGC ACAGGGTGCA GCAAGTAGTT GTGAAAAATG GGAAGATGTT TTAATTCAAA   360

CTATTAAGGC TATTAATAAT AGAGAAGATG TTTACATTGA AACTTCAAAC TTGCTGAAAC   420

ATAAAATACT CATTTATCCA CTAAATTCTG AACTTATTAA ATTTAAACCT AGCAAGTATA   480

TGCTACCTAC ACCGAATGAA CAAGTTGATA AAGACTCAAC CGATGTAGCT CTTCTACATT   540

GATTTTGTTT TGGGC   555

(2) INFORMATION FOR SEQ ID NO: 148:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 549 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GTTTCTTCTT GGAGAATTTT GATTTGAAGA TTTTGAATTT TGAGATTCAT TTTCAAGATT   60

TTGGTTATTT TCTGATGGAT TTTTTGTTGA ATTTCCTGTT AAATTTTCTG AATTGGTGTG   120

ATTGCTTGTG TTTTTTAGAT TTCTAGAATT GTTGCTTCGT TTTGTTTTTT TTAGACTTTT   180

AGAAGTGGTA GGATTTTTTG GTTCGTTTGG GTTAACATTG CCAAAAGGTG CACATGATAT   240

GCAAATTGAA GTTAATATTG CTGTAATAAC GTTAAGTTTA ATAATATTTA ATTTAAAGTT   300

TTTCAAAATA TTCTCCTTAT AAATTTGAAT TAATATTTAT TAATTTTAGT TCAAATATAT   360

AATATTACAA TTTAATATCA ATATCAAATA AGTTTAATAT TATTGATATT GAAAATTAAT   420

TTCATGAGTT TTAGCGGGAT TAGATGCATG AATTTAAAAA TAAAAGTAAT CTCCCTTTTA   480

AAATATGAAG TGnAACAATT GTTGGATTAA GGGGTTAATC CAGGAnCAGA GGGAATTAGA   540

AATATAACG   549

(2) INFORMATION FOR SEQ ID NO: 149:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 544 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TTTTGTAATT TTCATATTCA TTAATTAAAT GATAAGACTT CTTTTTTTAA TGaAAAATAA   60

TATTTCAAAA ATAAAATAAG CTCTTTTAGT ATCTTCTTTA CAAAATTCGT AAAACCCTTT   120

GTTTTTTATT AAAATCCTAA TAGACATTTT TCTATTATTT ACTTCAGGCA AATTTTCTTT   180

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TTTTTACGTT TGATAAATTC TCTTTTAACT GTCTTTGTAT TCCTCTAAAG CCCTATTTTT      240

TAATTTTATC TATATAAACA GGCCTCCTCT AAAACCCTTT TTCCGTAAAC TTTTTTTGCT      300

ATACTTTGTA TTAATAAATT TCCTAAAAGG AATTTTAAAA TTTTCTTTTA TTAAATCTTT      360

AAATACACTT TGATCTTCTT TTATACAAAG GGGAAATACA TGGCTTGATT CACTGCATCT      420

ATTTGAAACA AAACATCTCT ATAAAATTCT AGAGGTAAAA GAATGAAAAA AATTATTTGT      480

CGATAAAAAT CCTGTTGTAA TAAGGGTTAT ATTATTCTCn ATTTCCnAAA TATATTTTTT      540

TATA                                                                  544
```

(2) INFORMATION FOR SEQ ID NO: 150:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 533 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```
GAGACTTTGA AGCTATCTCG TCAGGGGTAG TGGAGTCAAT CTTGAAATAC CACCCTTGTT      60

TAATTAGGTT TCTAACTTAT AGAAATATGA GGAGAGTGCC AGGTGGGTAG TTTGACTGGG      120

GCGGTCGCCT CCTAAAGAGT AACGGAGGTG CGCAAAGGTT ACCTTAGAGT GGTTGGAAAT      180

CACTCTGTAA GTGTAAAGGC ATAAGGTAGC TTAACTGTAA GACTGACAAG TCGAACAGAT      240

ACGAAAGTAG GTCTTAGTGA TCTGGCGGTG GCAAGTGGAA GCGCCGTCAC TTAACGAATA      300

AAAGGTACTC CGGGGATAAC AGGCTTATCC TTCCCAAGAG TTCACATCGA CGGAAGGgTT      360

TGGCACcTCG ATGTCGGCTC ATCGCATCCT AGGGcTGGAG CAGgTCCTAA GGGTATGGCT      420

GTTCGCCATT TAAAGCGGTA CCGAGCTGGG TTCAGAACGT CGTGAGACAG TTTGGTCCCT      480

ATCTGCCACA AGCGTTGGAT ATTGAGAGGA GCTATnTTAG TACGAGAGGA CCG           533
```

(2) INFORMATION FOR SEQ ID NO: 151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 521 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
TGGTTTTGAA GCTTTTTTAG TAGGCTTAGA AGAAATTTTT AGTGAATTTT TAAGAATTTT      60

ATTTTCATTT AGCACATTTT GATAATCTTG AAATAGTTTG AGCATAAAAT CCATGTTGAA      120
```

```
ATTATTTAAA TTAAAATAAT TATTAGTGTT CATAAAATCC TCTCCTTGAA GGTGTTACTT      180

TTAAATTAAG TAAAAGTAAT AAAAATAGAT AAAAATAGTA ATTTATATTG TACCAAAAAC      240

GAAAAATTTT AGTCAAATTT TGTGAGTTCT CATTGCATGA GAAATTTGGG TTGTAGGGAG      300

GCTGTTATAA ATAGAATGGG CATTTTCTGA GGGTGTCGGC TAAGAAAGAC TACATACTTT      360

AGCTAATATA TAGCAAAGAC TTTGAAATTT AATTTGTATG TGTTTTATAG TCTTTTGTAA      420

TGAGTAGTGC ATTTGCAATG GAGAGATTTT GGGGAGTTGT TTAAAATTAC ATTTGCGTTT      480

TGTTAAAATG TAACAGCTGA ATGTAACAAA ATTATATATT T                          521
```

(2) INFORMATION FOR SEQ ID NO: 152:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 501 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
GTTCTCAAAT TTTTATAAAT CTTGTTTAGG AATTTTCTTT TTTTCTTTCA ATTGACTTTT      60

CTAATTTACG CTTTATGTAA CTTAGaTCGC TATATTTATG ATTTTCAATA ATAAAGTGGG      120

GTTTATATTT GTAATTTTCG TATATTTTTT GAAAATTTGT TTCTAATTGT TCTGAATTGT      180

ATCCACTTTT TTCTAATTCT TTTTGAGTGT TGCATAGAAT TTTCTTTAAT TTTTCTTGTT      240

TTTCTTTACT GCAAGATTTA GGAAAGTAAA TATTTTTATT TTTTGCTTTA ATATCAGTTC      300

TTTTTATGGT TTTAATTATT TTGATCATAG TATCTTaTCA ACATTTAAAT TTAATAAAAT      360

TGAAAGAATT tCTTTACATG AAAAGTTGCA TTtATtGAAA TAATTtATtA CTGATACTTT      420

CTATTcATTA AcCTTCTTCT cTTTATAtAt TTTATTACTA TTACAGGAnT CACACGTACA      480

CTACCCATTT TGAACCGAAT T                                                501
```

(2) INFORMATION FOR SEQ ID NO: 153:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 488 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
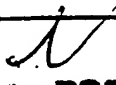

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
GTTCCnCnTT ATCAAGGAAA TTAACGACAT CTTTCATTAT GGTTTCATTT GCAAATTTAA      60
```

```
CAAAATTGTC TTTTTCTTTT TCTAATCTTT TTCTGAAGTT TTCAAATTCT GCTTGTTTTC        120

TTAAATACAA ATCTTTAAGA TTGGAGATTT CATTTTCAAG TTCAGCAATT TTTTTATCAG        180

AATTTACTAA ATTTAAGTTT TCTTTTTTTT GAGATTTTGT ATTTTTATTA TCTTGTTTGT        240

TGTTTTTTTC AGATTCGCTT TTAGTTTCTT TTTTTTCCAT TTTTCCTCCT kTGATAAAGC        300

ATTTTATCTT TAAAAAAAAT ATTTTACAAA TTTTnTTCTT TCytGAAATT TAAnAAAATG        360

GAGTCATTTT GnGGCATTTG TAAGATGTAG ATTTTTCTTA AGCTTTCAGT AAGAGTGTTA        420

TATGnATACA TAGGTTATTT AGTnAAAATG TTCGTGTGTA TTTTGTGTCA AAAGAAAAAA        480

TTTAAGTT                                                                 488
```

(2) INFORMATION FOR SEQ ID NO: 154:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 459 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
GGAGAGGCGG TTTGCGTATT GGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT         60

CGGTCGTTCG GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA        120

CAGAATCAGG ATAACGCAGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC        180

GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA        240

AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT        300

TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC        360

TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC TGTAGTATCT        420

CAGTTCGGTG TAGTCGTTCG CTCCAAGCTG GGCTGTGTG                               459
```

(2) INFORMATION FOR SEQ ID NO: 155:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 368 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
GAACAAGAGT CGAAAGTAGG TGTTAGTGAT sTGGCGGTGG CAAGTGGAAG CGCCGTCACT         60

TAACGAATAA AAGGTACTCC GGGGATAACA GGCTTATCCT TCCCAAGAGT TCACATCGAC        120
```

```
GGAAGGGTTT GGCACCTCGA TGTCGGCTCA TCGCATCCTA GGGCTGGAGC AGGTCCTAAG    180

GGTATGGCTG TTCGCCATTT AAAGCGGTAC GCrAGCTGGG TTCAGAACGT CGTGAGACAG    240

TTTGGTCCCT ATCTGCCACA AGCGTTGGAT ATTTGAGAGG AnCTATCTTT AGTACGAGAG    300

GACCGAGATG GACGAACCTC TAGTGTGCCA GTTATCCTGC CAAGGGTAAG TGCTGGGTAG    360

CTACnTTC                                                            368
```

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description
on page   **8**   . line   **23**

B. IDENTIFICATION OF DEPOSIT   Further deposits are identified on an additional sheet ___

Name of depositary institution

        American Type Culture Collection

Address of depositary institution (*including postal code and country*)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit August 8, 1997	Accession Number 202012

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)*   This information is continued on an additional sheet ___

EUROPE

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4)EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications. e.g. "Accession Number of Deposit"*)

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on ----
Authorized officer	Authorized officer
International Division RO/US ~(703)305-3600~	

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:

(a) any one nucleotide sequence of SEQ ID NOS:1-155; or

(b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).

(c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences of SEQ ID NOS:1-155; or,

(d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences of SEQ ID NOS:1-155.

2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.

3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.

4. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-155, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-155.

5. A method for making a recombinant vector comprising the step of inserting an isolated nucleic acid molecule of claim 1 into a vector.

6. A recombinant vector produced by the method of claim 5.

7. A host cell comprising the vector of claim 6.

8. A method of producing a polypeptide comprising:

(a) growing the host cell of claim 7 such that the protein is expressed by the cell; and

(b) recovering the expressed polypeptide.

9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:

(a) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155;

(b) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155 except the N-terminal residue;

(c) a fragment of the polypeptide of (a) having biological activity; and

(d) an epitope-bearing fragment of the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *B. burgdorferi* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A host cell which produces an antibody of claim 10.

16. A vaccine, comprising:

(1) one or more *B. burgdorferi* polypeptides selected from the group consisting of a polypeptide of claim 9; and

(2) a pharmaceutically acceptable diluent, carrier, or excipient;

wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Borrelia* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Borrelia* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Borrelia* nucleic acids in a biological sample comprising:

(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and

(b) detecting hybridization of said nucleic acids to the one or more *Borrelia* nucleic acid sequences present in the biological sample.

19. A method of detecting *Borrelia* nucleic acids in a biological sample obtained from an animal, comprising:

(a) amplifying one or more *Borrelia* nucleic acid sequences in said sample using polymerase chain reaction, and
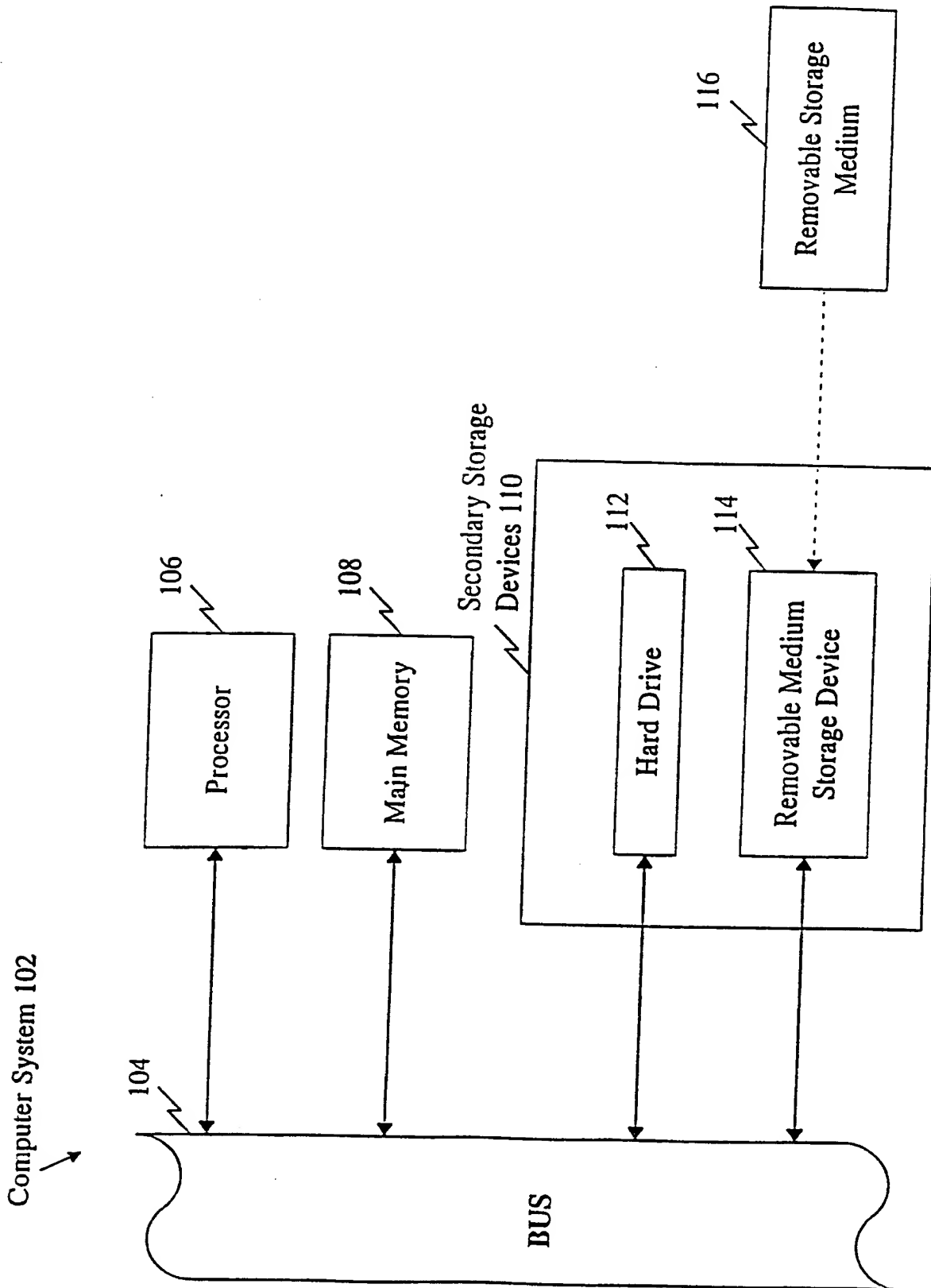
(b) detecting said amplified *Borrelia* nucleic acid.

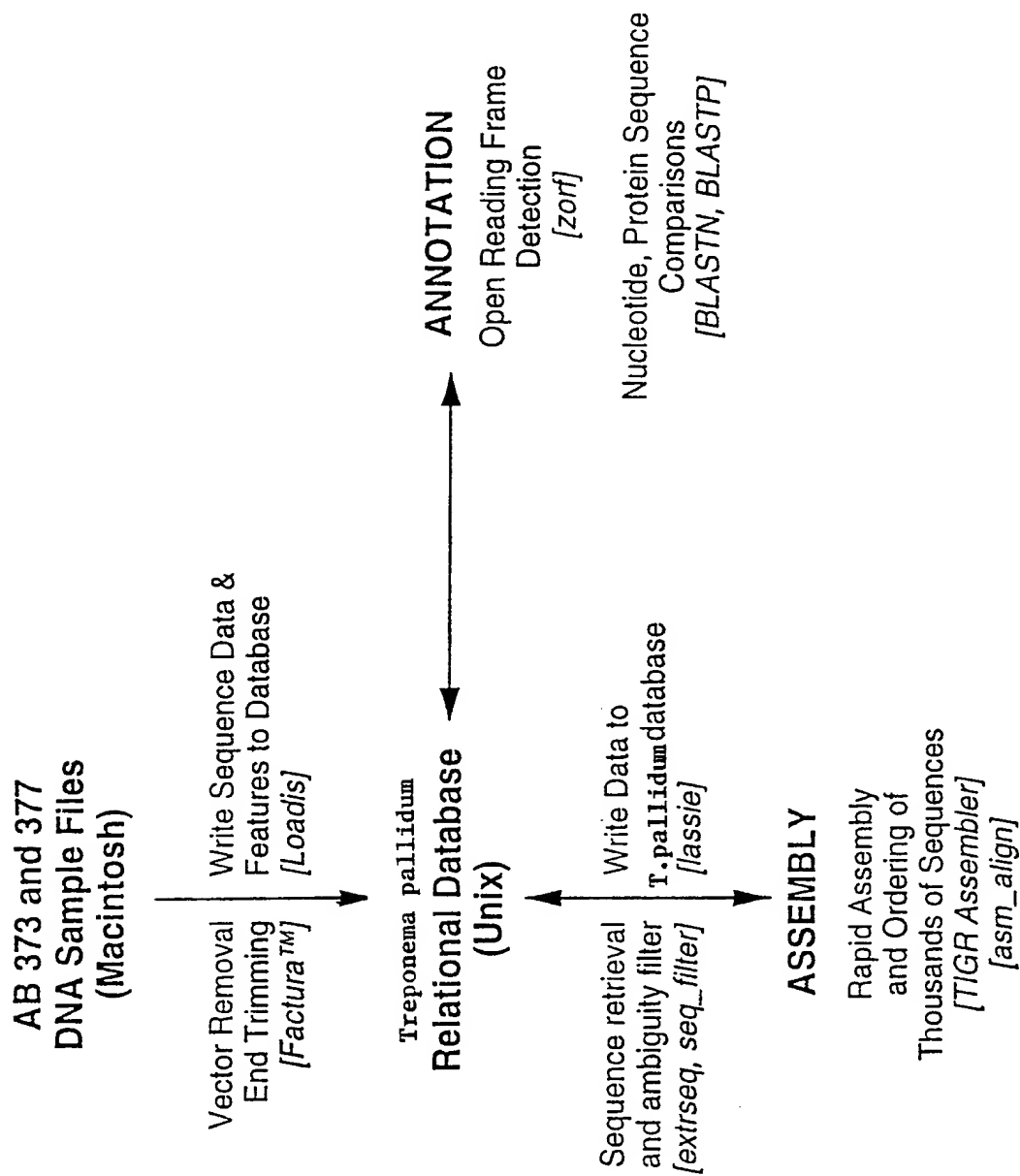20. A kit for detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) a polypeptide of claim 9 attached to a solid support; and

(b) detecting means.

21. A method of detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) contacting the sample with a polypeptide of claim 9; and

(b) detecting antibody-antigen complexes.

Figure 1

Figure 2

AB 373 and 377
DNA Sample Files
(Macintosh)

Vector Removal
End Trimming
[Factura™]

Write Sequence Data &
Features to Database
[Loadis]

Treponema pallidum
Relational Database
(Unix)

Sequence retrieval
and ambiguity filter
[extrseq, seq_filter]

Write Data to
T.pallidum database
[lassie]

ANNOTATION

Open Reading Frame
Detection
[zorf]

Nucleotide, Protein Sequence
Comparisons
[BLASTN, BLASTP]

ASSEMBLY

Rapid Assembly
and Ordering of
Thousands of Sequences
[TIGR Assembler]
[asm_align]

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/02, 2/04; C12N 5/00, 5/10, 15/00, 15/09, 15/11, 15/31
US CL :435/69.1, 71.1, 172.3; 536/23.1, 23.7. 24.3, 24.32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 71.1, 172.3; 536/23.1, 23.7. 24.3, 24.32

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

  Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BARBOUR, A.G. et al. The nucleotide sequence of a linear plasmid of Borrelia burgdorferi reveals similarities to those of circular plasmids of other prokaryotes. Journal of Bacteriology. 1996, Vol. 178, No. 22, pages 6635-6639, see entire document, especially sequences.	1-3, 5-8, and 14
Y,P	FRASER, C.M. et al. Genomic Sequence of a Lyme disease spirochaete, Borrelia burgdorferi. Nature. 11 December 1997, Vol. 390, pages 580-586, see entire document, especially sequences.	1-3, 5-8, and 14

☐ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
21 SEPTEMBER 1998	16 OCT 1998

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	BRIAN R. STANTON
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)★

INTERNATIONAL SEARCH REPORT

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: 4
   because they relate to subject matter not required to be searched by this Authority, namely:

   Please See Extra Sheet.

2. [ ] Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such
   an extent that no meaningful international search can be carried out, specifically:

3. [ ] Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

   Please See Extra Sheet.

1. [ ] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable
   claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
   of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers
   only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this international search report is
   restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
   1-3, 5-8, and 14

Remark on Protest   [ ] The additional search fees were accompanied by the applicant's protest.
                          [ ] No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)★

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

Databases: Genbank, APS
Search Terms: sequence search of claimed sequences including only first, middle, and last 100 bases of each of the first ten sequences; open; read?; frame?; orf; protein?; borrelia?

BOX I. OBSERVATIONS WHERE CLAIMS WERE FOUND UNSEARCHABLE
1. Subject matter not required to be searched by this ISA, namely:

The subject matter of claim 4 is directed to a "computer readable medium" having recorded thereon nucleotide sequence information. However, under PCT Rule 39, the International Searching Authority is not required to search an invention that is drawn to "mere presentations of information" (See Rule 39.1 (v)). Therefore, claim 4 has not been considered by this authority.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1.

Group I:

Claims 1-3, 5-8, and 14, drawn to a polynucleotide selected from SEQ ID NOs 1-155 and associated vectors, host cells, and methods of making proteins. This group includes the first method making the claimed vectors (claim 5) and the first method of use of the cells (claim 8) to make a product. There are a total of 155 polynucleotide sequences of which the first 10 are selected for examination and therefore, there are 37 remaining additional groups of 4 polynucleotide sequences.

Group II:

Claims 9, 11-13, and 16, drawn to polypeptides and/or fragments thereof with the amino acid sequence defined by SEQ ID NOs 1-155. Within this group there are a total of 155 polypeptide sequences and therefore 154 additional species of proteins.

Group III:

Claims 10 and 15, drawn to an antibody that binds to a polypeptide with the amino acid sequence defined by SEQ ID NOs:1-155. Within this group there are a total of 155 antibodies and therefore 154 additional species of antibody proteins.

Group IV:

Claim 17, drawn to a process of preventing, treating, or attenuating and infection caused by a member of the *Borrelia* genus by administering a polypeptide of group II which is a second/alternative process of use of the second product.

In Group IV, and where additional fees are paid, the claims are searched only insofar as they are applicable to the selected polypeptide as the first species as directed to a process practiced using a polypeptide. There are 154 additional polypeptide species of proteins.

Group V:

Claim 18 and 19, drawn to a method of detection of a *Borrelia* nucleic acid using the nucleic acids of the invention of group I. This method is a second process of use of the first claimed product in Group I. Additionally Group V contains indica that there are a total of 155 polynucleotide sequences and therefore, nine(9) additional groups of four (4) polynucleotide sequences beyond the first ten (10) sequences.

Group VI:

Claims 20 and 21, drawn to a method of detecting antibodies in biological samples using the proteins of the

invention of group II. This is an alternative process of use of the polypeptides. There appear to be a total of 155 polypeptide sequences and therefore 154 additional species of the use f these proteins.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Claims of Group I are drawn to nucleotides, nucleotide constructs, and/or methods requiring the use of nucleotides or nucleotide constructs that contain more than ten individual, independent, and distinct nucleotide sequences in alternative form. Accordingly, these claims are subject to lack of unity as outlined in 1192 O.G. 68 (19 November 1996).

For Group I, the first ten (10) of the individual polynucleotide sequences are designated as SEQ ID NOs 1-10. The search of the no more than ten sequences may include the complements of the selected sequences and, where appropriate, may include subsequences within the selected sequences (e.g., oligomeric probes and/or primers). Similarly, the invention of Group V encompasses the use of multiple independent and distinct proteins that are encompassed within the referenced O.G. notice.

In Group II-IV and VI (as directed to the species which are polynucleotides or antibodies) should applicant pay the additional fee for the examination/search of any of these inventions, additional fees will be required for consideration of each of the species of proteins and/or antibodies after the first of each.

Where Applicant may elect to pay additional fees for a search of sequences beyond the initial ten (10) polynucleotide sequences, and in accordance with 1192 O.G. 68 (19 November 1996), applicant may select additional groups of polynucleotides consisting of four (4) sequences beyond the initial ten (10) sequences for Group I which would then be searched with Group I upon payment of the requisite fees for the requisite Groups beyond Group I.

As to the polypeptides and antibodies of Groups II, III, IV and VI, (as directed to different species of polypeptides and antibodies) each is a distinct and different protein with no requisite structural or functional relationship.

The special technical feature of the invention of group I is directed to nucleic acids that are prepared from a bacterial genome. This special technical feature encompasses nucleic acids that are not *per se* required to encode proteins and may be used in multiple independent manners. For example, the nucleic acids may be used as probes to detect bacterial infections. In contrast, the special technical feature of the inventions of groups II-IV and VI encompass proteins and antibodies which are materially distinct molecules with no functional or structural relationship with the claimed nucleic acids. Similarly, multiple uses of the claimed nucleic acids are claimed (see groups I and V) and such bear no requisite structural linkage. For example, the invention of group I requires the use of nucleic acids that encode proteins whereas the invention of group v only requires that organisms contain sequences that hybridize with those claimed.

Therefore, the separately claimed compositions and methods of using such are not so linked by any single special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.